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OM protein - protein search, using sw model

Run on: January 4, 2005, 08:56:31 : Search time 39.6824 seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-9

Perfect score: 664

Sequence: 1 ALELVTLTGKIDGRQTLV.....AALLASPLLDALIDQNPAY 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_23sep04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	5	ABG94320
2	664	100.0	132	5	ABG80632
3	664	100.0	132	6	ABR56455
4	664	100.0	132	6	ABU09693
5	664	100.0	132	6	ABR44558
6	664	100.0	132	7	ADD24133
7	664	100.0	132	7	ADJ82059
8	664	100.0	132	7	ADK17147
9	664	100.0	132	8	ADJ36316
10	664	100.0	132	8	ADJ67162
11	664	100.0	132	8	ADK52196
12	661	99.5	132	5	ABG94319
13	661	99.5	132	5	ABG80631
14	661	99.5	132	6	ABR56456
15	661	99.5	132	6	ABU09692
16	661	99.5	132	6	ABR44559
17	661	99.5	132	7	ADD24134
18	661	99.5	132	7	ADJ82060
19	661	99.5	132	7	ADK17148
20	661	99.5	132	8	ADJ36317
21	661	99.5	132	8	ADJ67163
22	661	99.5	132	8	ADK52197
23	658	99.1	132	5	ABG94316
24	658	99.1	132	5	ABG80628
25	658	99.1	132	6	ABR56452

26	658	99.1	132	6	ABU09689	ABU09689 Bacterioph
27	658	99.1	132	6	ABR44555	ABR44555 Bacterioph
28	658	99.1	132	7	ADD24130	ADD24130 Bacterioph
29	658	99.1	132	7	ADJ82056	ADJ82056 Protein f
30	658	99.1	132	7	ADK17144	ADK17144 Virus-11k
31	658	99.1	132	8	ADJ36313	ADJ36313 Bacterioph
32	658	99.1	132	8	ADJ67159	ADJ67159 Phage Qbe
33	658	99.1	132	8	ADK52193	ADK52193 Bacterioph
34	655	98.6	132	5	ABG94223	ABG94223 Bacterioph
35	655	98.6	132	5	ABG94318	ABG94318 POB250 pr
36	655	98.6	132	5	ABG94317	ABG94317 POB243 pr
37	655	98.6	132	5	ABG80629	ABG80629 Bacterioph
38	655	98.6	132	5	ABG80630	ABG80630 Bacterioph
39	655	98.6	132	5	ABG80545	ABG80545 Bacterioph
40	655	98.6	132	6	ABR56454	ABR56454 Bacterioph
41	655	98.6	132	6	ABR56439	ABR56439 Bacterioph
42	655	98.6	132	6	ABR56453	ABR56453 Bacterioph
43	655	98.6	132	6	ABU09686	ABU09686 Bacterioph
44	655	98.6	132	6	ABU09690	ABU09690 Bacterioph
45	655	98.6	132	6	ABU09691	ABU09691 Bacterioph

ALIGNMENTS

RESULT 1

ID ABG94320 standard; protein; 132 AA.

AC ABG94320;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

XX POB251 protein.

XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;

XX cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;

XX vaccine; infectious disease.

XX unidentified bacteriophage.

XX WO200256905-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-IB000166.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326988P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;

XX Piossek C;

XX WPI; 2002-627351/67.

XX Molecular antigen array used in the production of vaccines for infectious

XX diseases.

XX Claim 18; Page 426; 441pp; English.

XX This invention relates to a novel ordered and repetitive antigen array

XX used in the production of vaccines for infectious diseases. The invention

XX also discloses a composition comprising a non-natural molecular scaffold

XX comprising a core particle selected from a core particle of a non-natural

XX origin and a core particle of natural origin and an organiser comprising

XX at least one first attachment site, where the organiser is connected to

XX the core particle by at least one covalent bond. Also disclosed is an

XX antigen or antigenic determinant with at least one second attachment

XX site.

XX

XX

XX

XX

XX

XX

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Obeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -Aug-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVQSPSRNRK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVQSPSRNRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120

QY 121 LTDAIDQINPAY 132
 DB 121 LTDAIDQINPAY 132

RESULT 2
 ABG80632
 ID ABG80632 standard; protein; 132 AA.

XX ABG80632;

DT 29-NOV-2002 (first entry)

DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-259.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic aschma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angiotumproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM zneumatocyst; cysteine-containing linker.

XX Bacteriophage Qbeta.
 OS Synthetic.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-IB000168.

XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326988P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEO) LUEBEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 PI Maurer P., Lechner F., Ortman R., Lucend R., Staufenbiel M., Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX WPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

PS Example 18; Page 146; 418p; English.

XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angiotumproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVQSPSRNRK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVQSPSRNRK 60

QY 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIOMPACTANGSCDPSVTRKXADVTFSFTQYSTDEBERAFVTEIAALLASPL 120

QY 121 LTDAIDQINPAY 132
 DB 121 LTDAIDQINPAY 132

RESULT 3
 ABR56455
 ID ABR56455 standard; protein; 132 AA.

XX ABR56455;
AC
XX 28-JUL-2003 (first entry)
DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:26.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KM cytotoxic; immunosuppressive; antiparasitic; fungicide;
KM antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
KM antihypertoid; antidiabetic; neuroprotective; nootropic; osteopathic;
KM antineuritic; antineuritic; vaccine; immunisation; infectious disease;
KM anti-neuritic; antineuritic; vaccine; immunisation; infectious disease;
KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KM inflammatory autoimmune disease.
XX Bacteriophage Qbeta.
OS Synthetic.
XX WO2003024480-A2.
XX
XX 27-MAR-2003.
XX
XX 16-SEP-2002; 2002WO-IB004252.
XX
XX 14-SEP-2001; 2001US-0318967P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M, Storni T, Lechner F;
XX
XX WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX Disclosure; Page 182; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
XX response against an antigen or a virus-like particle in an animal. (C)
XX comprises a virus-like particle (VLP) bound to at least one antigen, or a
XX VLP capable of being recognised by the immune system of the animal. Also
XX described: (1) enhancing an immune response against an antigen or a VLP
XX in an animal comprising introducing (C) into the animal; (2) vaccines
XX comprising (C) together with a pharmaceutical diluent, carrier or
XX excipient; (3) immunising or treating an animal comprising administering
XX the vaccine to the animal, or priming or boosting a T cell response in
XX the animal by administering the vaccine; and (4) enhancing anti-viral
XX protection in an animal comprising introducing (C) into the animal. (C)
XX has cytotoxic, virucide, antibacterial, antiparasitic, fungicide,
XX antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
XX antihypertoid, antidiabetic, neuroprotective, nootropic, osteopathic,
XX antineuritic and antineuritic activities. (C) or the vaccines can be
XX used for enhancing an immune response against an antigen or a VLP in an
XX animal, enhancing anti-viral protection in an animal, or immunising or
XX treating tumors and infectious diseases such as viral, bacterial,
XX parasitic or fungal infections. The vaccine compositions are also useful
XX for preventing or treating allergies, drug addiction, graft-versus-host
XX disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
XX Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
XX autoimmune disease. ACC5938 to ACC5982 and ABR56401 to ABR56509
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLETVTLAGNIGKDGQTLVLPNGVNPITNGVSLSQAGVPALEKRVTVSVSQPSNRK 60

DB 1 AKLETVTLAGNIGKDGQTLVLPNGVNPITNGVSLSQAGVPALEKRVTVSVSQPSNRK 60
QY 61 NYKVQYKIONPPTACTANGSCDPSVTRQKADYVFESTQVSTDEERA FVRELAALLASPL 120
DB 61 NYKVQYKIONPPTACTANGSCDPSVTRQKADYVFESTQVSTDEERA FVRELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132
RESULT 4
ABU09693 standard; protein; 132 AA.
ID ABU09693;
AC ABU09693;
XX
XX 03-JUL-2003 (first entry)
XX
XX Bacteriophage Qbeta mutant coat protein #5.
DE
XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
KM cardiant; nephroprotective; ophthalmological; immunostimulant; vaccine;
KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KM renin-activated angiotensin system; hypertension; stroke; infarction;
KM congestive heart failure; kidney failure; retinal haemorrhage; mutant;
KM mutein.
XX Bacteriophage Qbeta.
OS
XX WO2003031466-A2.
XX
XX 17-APR-2003.
XX
XX 07-OCT-2002; 2002WO-EP011219.
XX
XX 05-OCT-2001; 2001US-0326998P.
XX 07-NOV-2001; 2001US-0331045P.
XX 18-JAN-2002; 2002US-00050902.
XX 21-JAN-2002; 2002WO-IB000166.
XX 19-JUL-2002; 2002US-0396637P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M;
XX
XX WPI; 2003-430264/40.
XX
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety, useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
XX
XX Claim 20; Page 94; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate
XX comprising: (a) a carrier with at least one first attachment site; and
XX (b) at least one angiotensin peptide moiety with at least one second
XX attachment site. The angiotensin peptide moiety and compositions
XX comprising them are useful for immunising an animal against an
XX angiotensin peptide, and for treating or preventing a physical disorder
XX associated with renin-activated angiotensin system such as hypertension,
XX stroke, infarction, congestive heart failure, kidney failure, and retinal
XX hemorrhage. The conjugate is also useful for inducing immune responses,
XX including producing antibodies. This is the amino acid sequence of a
XX mutant bacteriophage Qbeta coat protein used in the preparation of the
XX vaccine conjugates of the invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
QY 1 AKLETVTLAGNIGKDGQTLVLPNGVNPITNGVSLSQAGVPALEKRVTVSVSQPSNRK 60

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRNK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRNK 60

QY 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBERAFVTEIAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 5
 ABR44558 standard; protein; 132 AA.

XX ABR44558;
 XX AC
 XX DT 25-JUL-2003 (first entry)
 XX

Bacteriophage Q-beta coat protein mutant SEQ ID NO:26.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; vituicide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX Bacteriophage Qbeta.
 OS Synthetic.
 OS WO2003024481-A2.

XX 27-MAR-2003.
 XX

16-SEP-2002; 2002MO-IB004132.
 XX

14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.
 XX

(CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER) MAURER P.
 PA (TISSOT) TISSOT A.
 PA (SCHWAB) SCHWAB K.
 PA (MEIJER) MEIJERINK E.
 PA (LIPPO) LIPPOMSKY G.
 PA (PUMPE) PUMPENS P.
 PA (CIELE) CIELENS I.
 PA (REINH) REINHOFER R.

XX MAURER P, TISSOT A, SCHWAB K, MEIJERINK E, LIPPOMSKY G,
 PI PUMPENS P, CIELENS I, REINHOFER R, Bachmann WF, Sornli T;
 XX WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX

XX Disclosure; Page 261-262; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, vituicide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer),
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.3e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRNK 60
 DB 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRNK 60

QY 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBERAFVTEIAALLASPL 120
 DB 61 NYKVQVKIONPACTANGSCDPSVTRQKXADVTFSTQYSTDEBERAFVTEIAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 6
 ADD24133 standard; protein; 132 AA.

XX ADD24133;
 XX

15-JAN-2004 (first entry)
 XX

Bacteriophage Qbeta coat protein mutant Qbeta-251.

XX vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; coat protein; mutant; mutein.

XX Synthetic.
 OS Bacteriophage Qbeta.
 OS WO2003059386-A2.

XX 24-JUL-2003.
 XX

17-JAN-2003; 2003MO-BP000460.
 XX

18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002MO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX

(CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER) MAURER P.
 PA (PELLEIOLI) PELLEIOLI E.
 PA (RENNER) RENNER WA;
 PI WPI; 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.

PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

PS Disclosure; SEQ ID NO 26; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (Prp) or its dimer, or a Prp peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is the amino acid sequence of a mutant coat protein from bacteriophage Qbeta which may be used during the creation of the vaccine composition of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEETVLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

DB 1 AKLEETVLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

QY 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFVTELAALLASPL 120

DB 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFVTELAALLASPL 120

QY 121 LIDAIQDQNPAY 132

DB 121 LIDAIQDQNPAY 132

RESULT 7

ADJ82059

ID ADJ82059 standard; protein; 132 AA.

AC ADJ82059;

DT 06-MAY-2004 (first entry)

DE Protein for RANKL antigen array to treat bone disease.

KW osteopathic; vaccine; core particle; antigenic determinant; RANKL; bone disease; encephalopathy; immune system stimulation.

XX Unidentified.

OS Unidentified.

PN WO2003039225-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012449.

XX 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Maurer P, Spohn G;

XX MPI; 2003-441430/41.

XX Disclosure; SEQ ID NO 26; 222pp; English.

XX The invention relates to a composition comprising a core particle having at least one first attachment site, and at least one antigen or antigenic determinant having at least one second attachment site. The antigen or antigenic determinant is a RANKL protein, RANKL fragment or RANKL peptide. The second attachment site is (non-) naturally occurring with the antigen or antigenic determinant, and is capable of association to the first attachment site. The antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The composition is useful as a medicament, or for the manufacture of a medicament for treating bone diseases. The composition is especially useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies, and for stimulating mammalian immune system. This sequence represents a protein of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEETVLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

DB 1 AKLEETVLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

QY 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFVTELAALLASPL 120

DB 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDEBRAFVTELAALLASPL 120

QY 121 LIDAIQDQNPAY 132

DB 121 LIDAIQDQNPAY 132

RESULT 8

ADK17147

ID ADK17147 standard; peptide; 132 AA.

AC ADK17147;

DT 06-MAY-2004 (first entry)

DE Virus-like particle repetitive antigen array peptide #26.

KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle; interleukin; IL-5; IL-13; ectaxin; repetitive antigen array; allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX Unidentified.

OS Unidentified.

PN WO2003040164-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012455.

XX 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Jennings G, Sonderregger I;

XX MPI; 2003-441518/41.

XX Composition comprising an ordered and repetitive antigen or antigenic determinant array, useful as a medicament, or for manufacturing a medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's lymphoma.
XX
XX
XX Disclosure; SEQ ID NO 26; 245pp; English.
CC The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC compositions are useful as medicaments, or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.
XX
XX Sequence 132 AA;
SQ
Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGKDGRTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSQPSRNK 60
Db 1 AKLEVTTLGNIGKDGRTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSQPSRNK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
Db 61 NYKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
QY 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 9
ADJ6316
ID ADJ6316 standard; protein; 132 AA.
XX
XX ADJ6316;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Bacteriophage Qbeta coat protein virus-like particle mutant K2RK13R.
DE
XX
XX antiallergic; cytostatic; virucide; immunostimulant; vaccine;
KM immune response; virus-like particle; immunostimulatory; allergy; tumour;
KM chronic disease; chronic viral disease; bacteriophage Qbeta;
KM coat protein; VLP; adjuvant; mutant; mutein.
XX
XX Bacteriophage Qbeta.
OS
XX
XX WO2004000351-A1.
PN
XX
XX 31-DEC-2003.
PD
XX
XX 20-JUN-2003; 2003WO-EP006541.
PF
XX
XX 20-JUN-2002; 2002US-0389898P.
PR
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA
XX
XX Bachmann MF, Renner WA;
PI
XX
XX WPI; 2004-108361/11.
DR
XX
XX New compositions comprising a virus-like particle (VLP), an
PT immunostimulatory substance bound to the VLP, and an antigen mixed with
PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
XX
XX
XX Disclosure; SEQ ID NO 17; 252pp; English.
PS
XX
XX The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC diseases such as allergies, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
CC coat protein mutant, a virus like particle (VLP) that can be used in the
CC adjuvant of the invention.
XX
XX Sequence 132 AA;
SQ
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGKDGRTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSQPSRNK 60
Db 1 AKLEVTTLGNIGKDGRTLVLPNGVNPNGVNSLSQAGAVPALERKRVTVSVSQPSRNK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
Db 61 NYKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
QY 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 10
ADJ67162
ID ADJ67162 standard; protein; 132 AA.
XX
XX ADJ67162;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Phage Qbeta coat protein mutant Qbeta 251 for antigen display array.
DE
XX
XX anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
KM antigenic array.
KM
XX
XX Bacteriophage Qbeta.
OS
XX
XX Synthetic.
OS
XX
XX WO2004009124-A2.
PN
XX
XX 29-JAN-2004.
PD
XX
XX 18-JUL-2003; 2003WO-EP007849.
PF
XX
XX 19-JUL-2002; 2002US-039638P.
PR
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA
XX
XX Bachmann MF, Fulurija A;
PI
XX
XX WPI; 2004-132866/13.
DR
XX
XX New composition comprising a core particle having a first attachment site
PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
PT peptide having a second attachment site, useful for treating obesity.
XX
XX Disclosure; SEQ ID NO 20; 175pp; English.
PS
XX
XX The invention relates to a new composition comprising: (i) a core
CC particle with at least one first attachment site; and (ii) at least one
CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin peptide, and where the second attachment site being consisting of an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association to the first attachment site, and where the ghrelin or a ghrelin peptide and the core particle interact through the association to form an ordered and repetitive antigen array. The composition is useful for treating obesity. The repetitive array may form part of a phage or bacterial display array. This peptide corresponds to a Bacteriophage Qbeta coat protein mutant which can be used as part of the repetitive or antigenic array.

Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.3e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0;

QY 1 AKLEVTTLGNIGDGRQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVQPSNRK 60

DB 1 AKLEVTTLGNIGDGRQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVQPSNRK 60

QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBRAFVRETLAALLASPL 120

DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBRAFVRETLAALLASPL 120

QY 121 LIDAIQOLNPAY 132

DB 121 LIDAIQOLNPAY 132

RESULT 11

ADK52196

ID ADK52196 standard; protein; 132 AA.

AC ADK52196;

DT 20-MAY-2004 (first entry)

XX Bacteriophage Qbeta coat protein mutant K16R A88K.

XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;

XX core particle; antigen array; Alzheimer's disease; RNA bacteriophage;

XX coat protein; CP; mutant; mutein.

OS Bacteriophage Qbeta.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 16

XX /note= "Wild type Lys substituted by Arg"

XX Misc-difference 88

XX /note= "Wild type Arg substituted by Lys"

XX WO2004016282-A1.

XX 26-FEB-2004.

XX 18-JUL-2003; 2003MO-EP007864.

XX 19-JUL-2002; 2002US-0396639P.

XX 15-MAY-2003; 2003US-0470432P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX (NOVS) NOVARTIS PHARMA AG.

XX Bachmann MF, Tisbet A, Ortman R, Lucend R, Staufenbiel M;

XX Frey P;

XX WPI, 2004-203731/19.

XX Composition comprising a core particle with at least one attachment site,

PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases

PT such as Alzheimer's disease.

XX Example 1; SEQ ID NO 20; 184bp; English.

XX The invention describes a novel composition comprising a virus-like core

XX particle with at least one attachment site, and an antigenic amyloid beta

XX 1-6 peptide. The new composition comprises: a core particle with at least

XX one first attachment site; and at least one antigen or antigenic

XX determinant with at least one second attachment site, where the antigen

XX or antigenic determinant is a Amyloid beta 1-6 peptide, and where the

XX second attachment site comprises: an attachment site not naturally

XX occurring with the antigen or antigenic determinant; or an attachment

XX site naturally occurring with the antigen or antigenic determinant. The

XX second attachment site is capable of association to the first attachment

XX site and the beta 1-6 peptide and the core particle interact through the

XX association to form an ordered and repetitive antigen array. The

XX composition is useful for the manufacture of a medicament for treating

XX of an RNA bacteriophage Qbeta coat protein mutant that can be used in the

XX preparation of the compositions and vaccines of the invention.

Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.3e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0;

QY 1 AKLEVTTLGNIGDGRQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVQPSNRK 60

DB 1 AKLEVTTLGNIGDGRQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVQPSNRK 60

QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBRAFVRETLAALLASPL 120

DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDEBRAFVRETLAALLASPL 120

QY 121 LIDAIQOLNPAY 132

DB 121 LIDAIQOLNPAY 132

RESULT 12

ABG94319

ID ABG94319 standard; protein; 132 AA.

AC ABG94319;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

XX PQB259 protein.

XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;

XX cytoskeletal; antiviral; antidiabetic; hypoglycaemic; antigen array;

XX vaccine; infectious disease.

XX unidentified bacteriophage.

XX WO200256905-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002MO-IB000166.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 07-OCT-2001; 2001US-0326998P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Renner WA, Bachmann M, Tisbet A, Maurer P, Lechner F, Seibel P;

XX Plosssek C;

XX WPI, 2002-627351/67.
 XX DR Molecular antigen array used in the production of vaccines for infectious
 XX PT diseases.
 XX PS Claim 18; Page 146; 441p; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organism comprising
 CC at least one first attachment site, where the organism is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (A-beta-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antibacterial, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)
 XX
 XX Sequence 132 AA;
 SQ
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 5.3e-71;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLETVTLGNIGKDGROTLVLPNGVPTNGVSLGAGVPLERKVTYSVQSPNRK 60
 Db 1 ARLETVTLGNIGKDGROTLVLPNGVPTNGVSLGAGVPLERKVTYSVQSPNRK 60
 QY 61 NYKQVXIQNPACTANGSCDPSTVRQKADVFPSFTQYSTDBERAFAVTELAALASPL 120
 Db 61 NYKQVXIQNPACTANGSCDPSTVRQKADVFPSFTQYSTDBERAFAVTELAALASPL 120
 QY 121 LIDAIQDLNPAY 132
 Db 121 LIDAIQDLNPAY 132

KW enterokinase; cysteine-containing linker.
 XX Bacteriophage Qbeta.
 OS Synthetic.
 XX WO200256907-A2.
 XX
 XX 25-JUL-2002.
 XX
 XX 21-JAN-2002; 2002WO-1E000168.
 XX
 XX 19-JAN-2001; 2001US-0262379P.
 XX 04-MAY-2001; 2001US-0288549P.
 XX 05-OCT-2001; 2001US-0326988P.
 XX 07-NOV-2001; 2001US-0331045P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEB) LUEBEND R.
 PA (STAUF) STAUFENBIEL M.
 PA (FREY) FREY P.
 XX
 XX Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX WPI, 2002-636514/68.
 XX
 XX Molecular antigen array used in the production of vaccines for infectious
 XX diseases.
 XX
 XX Example 18; Page 403; 418p; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organism comprising at least one first attachment
 CC site, where the organism is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (A-beta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, Igg-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 XX
 XX Sequence 132 AA;
 SQ
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 5.3e-71;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVSQPSRNRK 60
 DB 1 ARLETVTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVSQPSRNRK 60
 QY 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKYADVTFFSTQYSTDERAFVRETELAAALASPL 120
 DB 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKYADVTFFSTQYSTDERAFVRETELAAALASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132
 RESULT 14
 ABR56456
 ID ABR56456 standard; protein; 132 AA.
 AC ABR56456;
 XX
 XX 28-JUL-2003 (first entry)
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:27.
 XX
 XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytoelastic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antihydroid; antidiabetic; neuroprotective; nootropic; osteopathic;
 KW antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 XX Bacteriophage Qbeta.
 OS Synthetic.
 OS WO2003024480-A2.
 XX
 XX 27-MAR-2003.
 PD 16-SEP-2002; 2002WO-IB004252.
 PF 14-SEP-2001; 2001US-0318967P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann MF, Storni T, Lechner F;
 PI MPI; 2003-363095/34.
 XX
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 PT
 XX Disclosure; Page 183; 243pp; English.
 PS
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytoelastic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
 CC antihydroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antineumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an

CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumours and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 CC
 SO Sequence 132 AA:
 QY 1 AKLETVTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVSQPSRNRK 60
 DB 1 ARLETVTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVSQPSRNRK 60
 QY 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKYADVTFFSTQYSTDERAFVRETELAAALASPL 120
 DB 61 NYKVQVKIQNPPTACTANGSCDPSVTRQKYADVTFFSTQYSTDERAFVRETELAAALASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132
 RESULT 15
 ABU09692
 ID ABU09692 standard; protein; 132 AA.
 AC ABU09692;
 XX
 XX 03-JUL-2003 (first entry)
 DE Bacteriophage Qbeta mutant coat protein #4.
 XX
 XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.
 XX
 XX Bacteriophage Qbeta.
 OS
 XX WO2003031466-A2.
 XX
 XX 17-APR-2003.
 PD 07-OCT-2002; 2002WO-EP011219.
 PF 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M;
 PI MPI; 2003-430264/40.
 XX
 XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 PT
 XX Claim 20; Page 94; 97pp; English.
 PS
 XX The invention describes an angiotensin peptide moiety carrier conjugate

CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC mutant bacteriophage Obeta coat protein used in the preparation of the
CC vaccine conjugates of the invention

XX
SQ Sequence 132 AA;

Query Match 99.5%; Score 661; DB 6; Length 132;

Best Local Similarity 99.2%; Pred. No. 5.3e-71;

Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
|:|||||
Db 1 ARLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60

QY 61 NYKVQVKIONPFTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTELAAILASPL 120
|:|||||
Db 61 NYKVQVKIONPFTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTELAAILASPL 120

QY 121 LIDAIIDQLNPAY 132
|:|||||
Db 121 LIDAIIDQLNPAY 132

Search completed: January 4, 2005, 09:11:02
Job time : 40.6824 secs

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: January 4, 2005, 09:05:21 : Search time 10.3622 Seconds
(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-9
Perfect score: 664
Sequence: 1 ALEFVTLGNICKDGRQTLV.....AALLASPLLDALDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B COMB.pep:*
3: /cgn2_6/prodata/1/aa/6A COMB.pep:*
4: /cgn2_6/prodata/1/aa/6B COMB.pep:*
5: /cgn2_6/prodata/1/aa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.5	12.7	626	4 US-09-485-717-2	Sequence 2, Appl1
2	84.5	12.7	626	4 US-09-948-722-2	Sequence 2, Appl1
3	79.5	12.0	409	4 US-09-328-352-4249	Sequence 4249, Ap
4	74.5	11.2	916	4 US-09-252-991A-23637	Sequence 23637, A
5	71.5	10.8	383	3 US-09-045-186-2	Sequence 2, Appl1
6	71.5	10.8	384	1 US-08-232-144-4	Sequence 4, Appl1
7	71.5	10.8	384	2 US-08-555-268A-15	Sequence 15, Appl
8	71.5	10.8	384	3 US-09-200-673-15	Sequence 15, Appl
9	71.5	10.8	384	4 US-10-013-846-4	Sequence 4, Appl1
10	71.5	10.8	384	4 US-09-708-392-9	Sequence 9, Appl1
11	71.5	10.8	384	5 PCT-US93-05039-3	Sequence 3, Appl1
12	71.5	10.8	411	3 US-08-817-869-3	Sequence 3, Appl1
13	71.5	10.8	411	5 PCT-US95-14377-3	Sequence 3, Appl1
14	71.5	10.7	233	3 US-08-725-459B-45	Sequence 45, Appl
15	71.5	10.7	341	3 US-08-725-459B-44	Sequence 44, Appl
16	71.5	10.7	434	3 US-08-725-459B-42	Sequence 42, Appl
17	70.5	10.6	502	4 US-09-270-767-44620	Sequence 44620, A
18	69.5	10.5	129	1 US-08-090-148-1	Sequence 1, Appl1
19	69.5	10.4	766	4 US-09-538-092-216	Sequence 216, App
20	69.5	10.4	1073	4 US-09-206-942-49	Sequence 49, Appl
21	69.5	10.4	1079	4 US-09-206-942-47	Sequence 47, Appl
22	68.5	10.3	569	4 US-09-248-796A-20249	Sequence 20249, A
23	68.5	10.3	733	4 US-09-248-796A-16565	Sequence 16565, A
24	68.5	10.3	1036	2 US-08-720-484A-5	Sequence 5, Appl1
25	68.5	10.3	1036	3 US-08-953-823A-5	Sequence 5, Appl1
26	68.5	10.3	1036	4 US-09-398-239-5	Sequence 5, Appl1
27	68.5	10.3	1036	4 US-09-560-876A-5	Sequence 5, Appl1

28	68.5	10.3	1065	4 US-09-560-876A-6	Sequence 6, Appl1
29	68	10.2	316	4 US-09-270-767-43925	Sequence 43925, A
30	68	10.2	316	4 US-09-270-767-59331	Sequence 59331, A
31	68	10.2	345	3 US-08-856-253-7	Sequence 7, Appl1
32	68	10.2	933	3 US-08-293-728-2	Sequence 2, Appl1
33	68	10.2	933	3 US-09-421-868-2	Sequence 2, Appl1
34	68	10.2	936	4 US-08-956-171B-5249	Sequence 5249, Ap
35	68	10.2	936	4 US-08-781-986A-5249	Sequence 5249, Ap
36	67.5	10.2	1328	4 US-08-781-891-76	Sequence 76, Appl
37	67.5	10.2	1328	4 US-09-618-166-76	Sequence 76, Appl
38	67	10.1	632	4 US-09-976-594-41	Sequence 41, Appl
39	67	10.1	3892	4 US-09-328-352-5503	Sequence 5503, Ap
40	66.5	10.0	279	3 US-08-397-411-13	Sequence 13, Appl
41	66.5	10.0	424	3 US-09-173-581-7	Sequence 7, Appl1
42	66.5	10.0	424	3 US-09-420-915-7	Sequence 7, Appl1
43	66.5	10.0	428	3 US-09-134-001C-2885	Sequence 2885, Ap
44	66	9.9	1281	2 US-08-843-530B-6	Sequence 6, Appl1
45	66	9.9	1281	4 US-09-636-728-5	Sequence 5, Appl1

ALIGNMENTS

```

RESULT 1
US-09-485-717-2
; Sequence 2, Application US/09485717
; Patent No. 6673353
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan
; APPLICANT: Hess, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 16862PUS
; CURRENT APPLICATION NUMBER: US/09/485, 717
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: EP 97114614.7
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/EP98-05109
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2
Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best local Similarity 22.7%; Pred. No. 0.16;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KDGRLTLV-----NRGVNPTNGVSLSQGA-----VPALEKRV 48
DB 138 KDNREYIVVEKKKKSINONNADIQVNAISLTPALVKNSELVENQDPVLPVKRSL 197
QY 49 TVSVSPSRNRKRYKQVQKIONPTACANGSCDPVTR-----OKYADYFSTOYSTD 102
DB 198 TLSIDILPGMTNOKNKIVK--NAIKSNVNNVAVTLVERNKEKYAQAIPNVS---AKIDYD 252
QY 103 EERAFVTEILAA 114
DB 253 DEMAYSESQSLA 264

RESULT 2
US-09-948-722-2
; Sequence 2, Application US/0948722
; Patent No. 6776993
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan H. E.
; APPLICANT: Hess, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine

```

FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
OTHER INFORMATION: escape domain
US-09-948-722-2

Query Match
Best Local Similarity 12.7%; Score 84.5; DB 4; Length 626;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGKQTLV-----NPRGVNPTNGVSLSQAG-----VPALKRV 48
DB 138 KDGKQTLV-----NPRGVNPTNGVSLSQAG-----VPALKRV 197
QY 49 TVSVSOPSRNKNKYQVQKIONPACTANGSCDSVTR-----QKADVFSTQYSTD 102
DB 198 TVSDLPQMTNODKVIYK--NATKSNVNNVNTLVERMEKTAQAAVPMVS--AKIDYD 252
QY 103 EERAFVETELAA 114
DB 253 DEMAYSESQLIA 264

RESULT 3
US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match
Best Local Similarity 12.0%; Score 79.5; DB 4; Length 409;
Matches 35; Conservative 19; Mismatches 53; Indels 25; Gaps 6;

QY 7 TLGNIGKDGKQTLV-----PR-----GVNPTNGVSLSQAGVPLAKRVTV-SVSPS 56
DB 109 SLNFTKDVAGGRINANNVRNMLISPAVNVDTGTP-----IAKPNQTLTRDLAAG 163
QY 57 RNRKNKYQVQKIONPACTANGSCDSVTRQKXADVFSTQYSTDERRAFVETELAA 116
DB 164 RTGSN--ALAYRREGEFTNNALVENVETAKPYSEITF-----EAVESVETIAHMLK 213
QY 117 ASPLLDALDOL 128
DB 214 ASKQIUDDLPOL 225

RESULT 4
US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637

Query Match
Best Local Similarity 11.2%; Score 74.5; DB 4; Length 916;
Matches 28; Conservative 16; Mismatches 53; Indels 21; Gaps 4;

QY 9 GNIGKDG-----RQTLVNPGRVNPNGVSLSQAGVPLAKRVTVS-----QP 55
DB 789 GLLGEGGALRLAAIVQARRIDPFQGLAALPVGGGLPQLAQEDFAFGSLDQRYQA 848
QY 56 SRNRKNKYQVQKIONPACTANGSCDSVTRQKXADVFSTQYSTDERRAFVET 110
DB 849 EERGAETRAQESAHREHPCRSIEANADCPISADAGK-----PWITFSDSATRMALRT 901

RESULT 5
US-09-045-186-2
Sequence 2, Application US/09045186
Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Baez, Melvyn
TITLE OF INVENTION: RHBSUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 15
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-09-200-673-15

Query Match 10.8%; Score 71.5; DB 3; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVNTN-----GVA---SLSDAGVPALEKRVTVSVSPSRNRKNKYQVK 67
DB 138 RQTLINPRGWRPNRRHAYVGIWVLA VASSLPFLIYO--VMTDEPPQN----- 186
QY 68 IQNPACTANGSCDPSVTRQKYADVTFSTFOYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKYVCDFQPSDSHRSLTYTLTLVL 218

RESULT 9

US-10-013-846-4
Sequence 4; Application US/10013846
Patent No. 6566367
GENERAL INFORMATION:
APPLICANT: Baktahavatchalam, Rajagopal
APPLICANT: Blum, Charles A
APPLICANT: Brielmann, Harry L
APPLICANT: Darrow, James W
APPLICANT: De Lombaert, Stephane
APPLICANT: Hutchinson, Alan
APPLICANT: Tran, Jennifer
APPLICANT: Zheng, Xiaozhang
APPLICANT: Elliott, Richard L
APPLICANT: Hammond, Marlys
TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
TITLE OF INVENTION: 3H-spiro[isobenzofuran-1,4'-piperidines
FILE REFERENCE: N00.2001
CURRENT APPLICATION NUMBER: US/10/013.846
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,990
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln version 3.1
SEQ ID NO 4
LENGTH: 384
TYPE: PRT
ORGANISM: homosapiens
US-10-013-846-4

Query Match 10.8%; Score 71.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVNTN-----GVA---SLSDAGVPALEKRVTVSVSPSRNRKNKYQVK 67
DB 138 RQTLINPRGWRPNRRHAYVGIWVLA VASSLPFLIYO--VMTDEPPQN----- 186
QY 68 IQNPACTANGSCDPSVTRQKYADVTFSTFOYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKYVCDFQPSDSHRSLTYTLTLVL 218

RESULT 10

US-09-708-392-9
Sequence 9; Application US/09708392
Patent No. 6734186
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Wayman, Chris
APPLICANT: Maw, G

TITLE OF INVENTION: Pharmaceutical
FILE REFERENCE: PCI0343AAM
CURRENT APPLICATION NUMBER: US/09/708,392
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: GB 9926437.6
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: GB 0004021.2
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GB 0013001.3
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 0016563.9
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: GB 0017141.3
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/217,479
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: US 60/221,014
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/221,093
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 9
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-09-708-392-9

Query Match 10.8%; Score 71.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVNTN-----GVA---SLSDAGVPALEKRVTVSVSPSRNRKNKYQVK 67
DB 138 RQTLINPRGWRPNRRHAYVGIWVLA VASSLPFLIYO--VMTDEPPQN----- 186
QY 68 IQNPACTANGSCDPSVTRQKYADVTFSTFOYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKYVCDFQPSDSHRSLTYTLTLVL 218

RESULT 11

PCT-US93-05039-3
Sequence 3; Application PC/TUS9305039
GENERAL INFORMATION:
APPLICANT: Claes R. Wallestedt
TITLE OF INVENTION: Human Neuropeptide Y/peptide YY
TITLE OF INVENTION: Receptor of the Y1-Type and
TITLE OF INVENTION: Antisense Oligonucleotides
TITLE OF INVENTION: Thereto Which Inhibit Vasoconstriction
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05039
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-05039-3

Query Match 10.8%; Score 71.5; DB 5; Length 384;
Best Local Similarity 25.9%; Pred. No.3.2; Indels 35; Gaps 4;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRVTVSVQPSNRNRKQYQVK 67
DB 138 RHQLINPGRMRRNNHAYGVIAVWLA VASSLPFLIYQ--VMTDEPFQN----- 186
QY 68 IQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKYVCDFQPSDSHRLSYTLLVL 218

RESULT 12
US-08-817-869-3
; Sequence 3, Application US/08817869
; Patent No. 6001970
; GENERAL INFORMATION:
; APPLICANT: STRADER, CATHERINE D.
; APPLICANT: CASCIERI, MARGARET A.
; APPLICANT: MACNEIL, DOUGLAS J.
; TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM H. NICHOLSON
; STREET: 126 EAST LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,017
; FILING DATE: 07-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NICHOLSON, WILLIAM H.
; REGISTRATION NUMBER: 25,147
; REFERENCE/DOCKET NUMBER: 19339Y PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732) 594-1348
; TELEFAX: (732) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-817-869-3

Query Match 10.8%; Score 71.5; DB 3; Length 411;

Best Local Similarity 25.9%; Pred. No.3.6;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;
QY 16 RQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRVTVSVQPSNRNRKQYQVK 67
DB 141 RHQLINPGRMRRNNHAYGVIAVWLA VASSLPFLIYQ--VMTDEPFQN----- 189
QY 68 IQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAAL 115
DB 190 -----VTLDAYKDKYVCDFQPSDSHRLSYTLLVL 221

RESULT 13
PCT-US95-14377-3
; Sequence 3, Application PC/TUS9514377
; GENERAL INFORMATION:
; APPLICANT: STRADER, CATHERINE D.
; APPLICANT: CASCIERI, MARGARET A.
; APPLICANT: MACNEIL, DOUGLAS J.
; TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APOLLINA
; STREET: 126 EAST LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,017
; FILING DATE: 07-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19339Y PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3462
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-14377-3

Query Match 10.8%; Score 71.5; DB 5; Length 411;
Best Local Similarity 25.9%; Pred. No.3.6; Indels 35; Gaps 4;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;
QY 16 RQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRVTVSVQPSNRNRKQYQVK 67
DB 141 RHQLINPGRMRRNNHAYGVIAVWLA VASSLPFLIYQ--VMTDEPFQN----- 189
QY 68 IQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAAL 115
DB 190 -----VTLDAYKDKYVCDFQPSDSHRLSYTLLVL 221
RESULT 14
US-08-725-459B-45
; Sequence 45, Application US/08725459B
; Patent No. 6084068

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/ GENERAL INFORMATION:
/ APPLICANT: CONAWAY, RONALD C.
/ APPLICANT: CONAWAY, JOAN W.
/ TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
/ NUMBER OF SEQUENCES: 79
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: SIDLEY & AUSTIN
/ STREET: 717 N. HARWOOD, SUITE 3400
/ CITY: DALLAS
/ STATE: TX
/ COUNTRY: US
/ ZIP: 75201-6507
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/725,459B
/ FILING DATE: 04-OCT-1996
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HANSEN, EUGENIA S.
/ REGISTRATION NUMBER: 31,966
/ REFERENCE/DOCKET NUMBER: 11146/07501
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 214-981-3300
/ TELEFAX: 214-981-3400
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 233 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..233
/ OTHER INFORMATION: /note="amino acids 202-434 of C.
/ OTHER INFORMATION: elegans"
/ US-08-725-459B-45

Query Match 10.7%; Score 71; DB 3; Length 233;
Best Local Similarity 33.7%; Pred. No. 1.7;
Matches 32; Conservative 11; Mismatches 38; Indels 14; Gaps 5;

QY 2 KLETVTLGNIGK-----DGRQTLVLPNGVNPFGVSLSQAGV--PALEKRVTVSVS 53
DB 116 KLEMLT-SRIGKNSAQSQRQTMVIDMAHTR---VRSKSPFTYKDSQVKMSATPPSAL 170
QY 54 QPSRNRKNYKVQYKIQNPACTANGSCDPSVTRQK 88
DB 171 QLSQARKNVKIEGKAQLRT-ITPRGGGVPTSRSR 204

RESULT 15
US-08-725-459B-44
/ Sequence 44; Application US/08725459B
/ Patent No. 6084068
/ GENERAL INFORMATION:
/ APPLICANT: CONAWAY, RONALD C.
/ APPLICANT: CONAWAY, JOAN W.
/ TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
/ NUMBER OF SEQUENCES: 79
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: SIDLEY & AUSTIN
/ STREET: 717 N. HARWOOD, SUITE 3400
/ CITY: DALLAS
/ STATE: TX
/ COUNTRY: US
/ ZIP: 75201-6507
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/725,459B
/ FILING DATE: 04-OCT-1996
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HANSEN, EUGENIA S.
/ REGISTRATION NUMBER: 31,966
/ REFERENCE/DOCKET NUMBER: 11146/07501
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 214-981-3300
/ TELEFAX: 214-981-3400
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 341 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..341
/ OTHER INFORMATION: /note="amino acids 94-434 of C.
/ OTHER INFORMATION: elegans"
/ US-08-725-459B-44

Query Match 10.7%; Score 71; DB 3; Length 341;
Best Local Similarity 33.7%; Pred. No. 3.1;
Matches 32; Conservative 11; Mismatches 38; Indels 14; Gaps 5;

QY 2 KLETVTLGNIGK-----DGRQTLVLPNGVNPFGVSLSQAGV--PALEKRVTVSVS 53
DB 224 KLEMLT-SRIGKNSAQSQRQTMVIDMAHTR---VRSKSPFTYKDSQVKMSATPPSAL 278
QY 54 QPSRNRKNYKVQYKIQNPACTANGSCDPSVTRQK 88
DB 279 QLSQARKNVKIEGKAQLRT-ITPRGGGVPTSRSR 312
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Search completed: January 4, 2005, 09:35:45
Job time: 11.3622 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-9

Perfect score: 664
Sequence: 1 AKLEVTLLGNIGKDGQTLV.....AALLASPLTIDAIDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
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- 4: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	664	100.0	132	14	US-10-243-739-26
2	664	100.0	132	14	US-10-244-065-26
3	664	100.0	132	14	US-10-289-454-26
4	664	100.0	132	14	US-10-050-902-259
5	664	100.0	132	14	US-10-050-898-259
6	664	100.0	132	14	US-10-346-190-26
7	664	100.0	132	15	US-10-465-811-17
8	664	100.0	132	15	US-10-289-456-26
9	664	100.0	132	15	US-10-622-064-9
10	664	100.0	132	15	US-10-622-124-20
11	664	100.0	132	16	US-10-622-087-20
12	661	99.5	132	14	US-10-243-739-27
13	661	99.5	132	14	US-10-244-065-27

14	661	99.5	132	14	US-10-289-454-27	Sequence 27, Appl
15	661	99.5	132	14	US-10-050-902-258	Sequence 258, App
16	661	99.5	132	14	US-10-050-898-258	Sequence 26, App
17	661	99.5	132	14	US-10-346-190-27	Sequence 27, Appl
18	661	99.5	132	15	US-10-465-811-18	Sequence 18, Appl
19	661	99.5	132	15	US-10-289-456-27	Sequence 27, Appl
20	661	99.5	132	15	US-10-622-064-10	Sequence 21, Appl
21	661	99.5	132	15	US-10-622-124-21	Sequence 21, Appl
22	661	99.5	132	16	US-10-622-087-21	Sequence 23, Appl
23	661	99.5	132	14	US-10-243-739-23	Sequence 23, Appl
24	661	99.5	132	14	US-10-244-065-23	Sequence 23, Appl
25	661	99.5	132	14	US-10-289-454-23	Sequence 23, Appl
26	661	99.5	132	14	US-10-050-902-255	Sequence 255, App
27	661	99.5	132	14	US-10-050-898-255	Sequence 255, App
28	661	99.5	132	14	US-10-346-190-23	Sequence 23, Appl
29	661	99.5	132	15	US-10-465-811-14	Sequence 14, Appl
30	661	99.5	132	15	US-10-289-456-23	Sequence 23, Appl
31	661	99.5	132	15	US-10-622-064-6	Sequence 6, Appl
32	661	99.5	132	14	US-10-622-124-17	Sequence 17, Appl
33	661	99.5	132	16	US-10-622-087-17	Sequence 17, Appl
34	661	99.5	132	14	US-10-243-739-10	Sequence 10, Appl
35	661	99.5	132	14	US-10-243-739-24	Sequence 24, Appl
36	661	99.5	132	14	US-10-243-739-25	Sequence 25, Appl
37	661	99.5	132	14	US-10-244-065-10	Sequence 10, Appl
38	661	99.5	132	14	US-10-244-065-24	Sequence 24, Appl
39	661	99.5	132	14	US-10-244-065-25	Sequence 25, Appl
40	661	99.5	132	14	US-10-289-454-10	Sequence 10, Appl
41	661	99.5	132	14	US-10-289-454-24	Sequence 24, Appl
42	661	99.5	132	14	US-10-289-454-25	Sequence 25, Appl
43	661	99.5	132	14	US-10-050-902-259	Sequence 159, App
44	661	99.5	132	14	US-10-050-902-256	Sequence 256, App
45	661	99.5	132	14	US-10-050-902-257	Sequence 257, App

ALIGNMENTS

RESULT 1
US-10-243-739-26
; Sequence 26, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243, 739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318, 967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 26
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTLLGNIGKDGQTLVLPNGVNPNGVNASLSQAQAVPALERKVVVSQPSRRNK 60
DB 1 AKLEVTLLGNIGKDGQTLVLPNGVNPNGVNASLSQAQAVPALERKVVVSQPSRRNK 60
QY NYKVQKINPNPACTANGSCDPSVTROKXADYVTSFTQSTDEERAFVTELAALASPL 120
DB 61 NYKVQKINPNPACTANGSCDPSVTROKXADYVTSFTQSTDEERAFVTELAALASPL 120
QY 121 LIDAIDQLNPAY 132

Db 121 LIDAIIDQLNPAY 132

RESULT 2

US-10-244-065-26
; Sequence 26, Application US/10244065
; Publication No. US2003009668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornil, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
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DB 61 NYKVQYKIONPRACTANGSCDPSVTROKYADVTFFSTQYSTDEBERAFVTEIAALLASPL 120
QY 121 LIDAIIDQLNPAY 132
DB 121 LIDAIIDQLNPAY 132

RESULT 3

US-10-289-454-26
; Sequence 26, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Uemlings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.036001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 26
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta-251
US-10-289-454-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AKLEVTTLNIGDGRQTLVLPNGVPTNGVASLSQAQAVPALERKVTVSQPSRNK 60
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DB 61 NYKVQYKIONPRACTANGSCDPSVTROKYADVTFFSTQYSTDEBERAFVTEIAALLASPL 120
QY 121 LIDAIIDQLNPAY 132
DB 121 LIDAIIDQLNPAY 132

RESULT 4

US-10-050-902-259
; Sequence 259, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 259
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 251
US-10-050-902-259

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 NYKVQYKIONPRACTANGSCDPSVTROKYADVTFFSTQYSTDEBERAFVTEIAALLASPL 120
QY 121 LIDAIIDQLNPAY 132
DB 121 LIDAIIDQLNPAY 132

RESULT 5
US-10-050-898-259
; Sequence 259, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Ploesek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Steufendiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 259
; LENGTH: 132
; TYPE: PR
; ORGANISM: Qb 251
US-10-050-898-259

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Best Local Similarity 100.0%; Pred. No. 1.6e-66;
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DB 61 NYKVQVKIQNPITACTANGSCDPSVTRQKADVTFSTQYSTDERAFVRTLAALLASPL 120

QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 6
US-10-346-190-26
; Sequence 26, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 132
; TYPE: PR
; ORGANISM: Qb 251
US-10-346-190-26

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKETVTLGNIGKDGROTLVLPNGVNPPTNGVSLSOAGAVPALERKVTYSVQPSNRK 60
DB 1 AKETVTLGNIGKDGROTLVLPNGVNPPTNGVSLSOAGAVPALERKVTYSVQPSNRK 60

QY 61 NYKVQVKIQNPITACTANGSCDPSVTRQKADVTFSTQYSTDERAFVRTLAALLASPL 120
DB 61 NYKVQVKIQNPITACTANGSCDPSVTRQKADVTFSTQYSTDERAFVRTLAALLASPL 120

QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 7
US-10-465-811-17
; Sequence 17, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 132
; TYPE: PR
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
US-10-465-811-17

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AKETVTLGNIGKDGROTLVLPNGVNPPTNGVSLSOAGAVPALERKVTYSVQPSNRK 60

QY 61 NYKVQVKIQNPITACTANGSCDPSVTRQKADVTFSTQYSTDERAFVRTLAALLASPL 120
DB 61 NYKVQVKIQNPITACTANGSCDPSVTRQKADVTFSTQYSTDERAFVRTLAALLASPL 120

QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 8
US-10-289-456-26
; Sequence 26, Application US/10289456

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: Publication No. US20040033211A1
: GENERAL INFORMATION:
: APPLICANT: Bachmann, Martin
: APPLICANT: Maurer, Patrick
: APPLICANT: Spohn, Gunther
: TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
: FILE REFERENCE: 1700.0330001
: CURRENT APPLICATION NUMBER: US/10/289,456
: PRIOR FILING DATE: 2002-11-07
: PRIOR APPLICATION NUMBER: PCT/IB02/00166
: PRIOR FILING DATE: 2002-01-21
: PRIOR APPLICATION NUMBER: US 10/050,902
: PRIOR FILING DATE: 2002-01-18
: PRIOR APPLICATION NUMBER: US 60/396,635
: PRIOR FILING DATE: 2002-07-19
: PRIOR APPLICATION NUMBER: US 60/331,045
: PRIOR FILING DATE: 2001-11-07
: NUMBER OF SEQ ID NOS: 170
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 26
: LENGTH: 132
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Q-beta 251 mutant
: US-10-289-456-26

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Db	1	AKLETVTLTGNIGKDGKQRTLVLPNRCVNPPTNGVASLSQAGAVPALEKRYTVSVSOPESRNKK	60	
QY	61	NYKQVAKIQNPACTANGSCDPSVTRQKADYTBFSFTQYSTDERRAFVTELTALLASPL	120	
Db	61	NYKQVAKIQNPACTANGSCDPSVTRQKADYTBFSFTQYSTDERRAFVTELTALLASPL	120	
QY	121	LIDAIIDQLNPAY	132	
Db	121	LIDAIIDQLNPAY	132	

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RESULT 9
US-10-622-064-9
; Sequence 9, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatencIn version 3.2
; SEQ ID NO 9
; LENGTH: 132
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
US-10-622-064-9

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Query Match      100.0%; Score 664; DB 15; length 132;
Beet Local Similarity 100.0%; Pred. No. 1,6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AKLEVTTLGNIGKDKOROTLVLPNGVPTNGIASISQAGAVPALEKRTVYSVSQPSRRK 60
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```

```

Db 1 AKETFTLGNIGDGSGQTVLNPRGVNPTNGVASLSQAGVPALEKVTWSVSPSNNRK 60
QY 61 NRYGVKINPTACTANGSCDPSTVRKRYKADVTSTFYSTDEERAFVRELATLALSPL 120
Db 61 NRYGVKIQINPTACTANGSCDPSTVRKRYKADVTSTFYSTDEERAFVRELATLALSPL 120
QY 121 LIDAIQQLNPAY 132
Db 121 LIDAIQQLNPAY 132

```

```

RESULT 10
US-10-622-124-20
? Sequence 20, Application US/10622124
? Publication No. US20040076645A1
? GENERAL INFORMATION:
? APPLICANT: Bachmann, Martin F
? TITLE OF INVENTION: Glycolin-Carrier Conjugates
? FILE REFERENCE: 1700.0340001
? CURRENT APPLICATION NUMBER: US/10/622,124
? CURRENT FILING DATE: 2003-07-18
? PRIOR APPLICATION NUMBER: US 60/396,638
? PRIOR FILING DATE: 2002-07-19
? NUMBER OF SEQ ID NOS: 146
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 20
? LENGTH: 132
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
US-10-622-124-20

```

Query March 132	100.0%	Score 664	DB 15	Length 132
Best Local Similarity	100.0%	Pred. No. 1.6e-66		
Matches 132	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	AKLEETLLGNIGKDGROTLVLPNGVPTNPGVASISQAGVPALEKRVTVSVSOPSNRK	60	
Db	1	AKLEETLLGNIGKDGQTLVLPNGVPTNPGVASISQAGVPALEKRVTVSVSOPSNRK	60	
QY	61	NYKVQKIONPIACTNAGSCDPSVTRQKYADVTG9FTQYSDERAAVRELAALLASPL	120	
Db	61	NYKVQKIONPIACTNAGSCDPSVTRQKYADVTG9FTQYSDERAAVRELAALLASPL	120	
QY	121	LIDAIQOLNPAY 132		
Db	121	LIDAIQOLNPAY 132		

```

RESULT 11
US-10-622-087-20
Sequence 20, Application US/10622087
Publication No. US20040141984A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tisoeot, Alain
APPLICANT: Ortmann, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Staufendiel, Matthias
APPLICANT: Frey, Peter
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,639
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/470,432
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20

```


LENGTH: 132.
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Bacteriophage Q-beta 251 mutant
 US-10-622-087-20

Query Match 100.0%; Score 664; DB 16; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.6e-66;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 ARLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 QY 61 NYKVQVQIQNPACTANGSCDPSVTRKQYADVTFSTQYSTDERAFVRETELAAALSPL 120
 DB 61 NYKVQVQIQNPACTANGSCDPSVTRKQYADVTFSTQYSTDERAFVRETELAAALSPL 120

QY 121 LIDALDQNLNPA 132
 DB 121 LIDALDQNLNPA 132

RESULT 12
 US-10-243-739-27
 Sequence 27, Application US/10243739
 Publication No. US20030091593A1
 GENERAL INFORMATION:
 APPLICANT: Bachmann, Martin F.
 APPLICANT: Storn, Tazio
 APPLICANT: Lechner, Franziska
 TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
 TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
 FILE REFERENCE: 1700.0210001
 CURRENT APPLICATION NUMBER: US/10/243.739
 CURRENT FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 60/318,967
 PRIOR FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 27
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Bacteriophage Q-beta
 US-10-243-739-27

Query Match 99.5%; Score 661; DB 14; Length 132;
 Best Local Similarity 99.2%; Pred. No. 3.5e-66;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 ARLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 QY 61 NYKVQVQIQNPACTANGSCDPSVTRKQYADVTFSTQYSTDERAFVRETELAAALSPL 120
 DB 61 NYKVQVQIQNPACTANGSCDPSVTRKQYADVTFSTQYSTDERAFVRETELAAALSPL 120
 QY 121 LIDALDQNLNPA 132
 DB 121 LIDALDQNLNPA 132

RESULT 13
 US-10-244-065-27
 Sequence 27, Application US/10244065
 Publication No. US20030099668A1
 GENERAL INFORMATION:
 APPLICANT: Bachmann, Martin F.
 APPLICANT: Storn, Tazio
 APPLICANT: Maurer, Patrick
 APPLICANT: Tissot, Alain

APPLICANT: Schwarz, Katrin
 APPLICANT: Meijerink, Edwin
 APPLICANT: Lipowsky, Gerard
 APPLICANT: Pumpens, Paul
 APPLICANT: Cielens, Indulis
 APPLICANT: Renhota, Regina
 TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
 TITLE OF INVENTION: Method of Preparation and Use
 FILE REFERENCE: 1700.0230001
 CURRENT APPLICATION NUMBER: US/10/244.065
 CURRENT FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 60/374,145
 PRIOR FILING DATE: 2002-04-22
 PRIOR APPLICATION NUMBER: 60/318,994
 PRIOR FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 27
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Bacteriophage Q-beta
 US-10-244-065-27

Query Match 99.5%; Score 661; DB 14; Length 132;
 Best Local Similarity 99.2%; Pred. No. 3.5e-66;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 ARLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 QY 61 NYKVQVQIQNPACTANGSCDPSVTRKQYADVTFSTQYSTDERAFVRETELAAALSPL 120
 DB 61 NYKVQVQIQNPACTANGSCDPSVTRKQYADVTFSTQYSTDERAFVRETELAAALSPL 120
 QY 121 LIDALDQNLNPA 132
 DB 121 LIDALDQNLNPA 132

RESULT 14
 US-10-289-454-27
 Sequence 27, Application US/10289454
 Publication No. US20030157479A1
 GENERAL INFORMATION:
 APPLICANT: Demings, Gary
 APPLICANT: Sonderegger, Ivo
 TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
 FILE REFERENCE: 1700.0360001
 CURRENT APPLICATION NUMBER: US/10/289.454
 CURRENT FILING DATE: 2003-02-10
 PRIOR APPLICATION NUMBER: US 60/396,636
 PRIOR FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: PCT/IB02/00166
 PRIOR FILING DATE: 2002-01-21
 PRIOR APPLICATION NUMBER: US 10/050,902
 PRIOR FILING DATE: 2002-01-18
 PRIOR APPLICATION NUMBER: US 60/331,045
 PRIOR FILING DATE: 2001-11-07
 NUMBER OF SEQ ID NOS: 386
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 27
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Bacteriophage Q-beta-259
 US-10-289-454-27

Query Match 99.5%; Score 661; DB 14; Length 132;
 Best Local Similarity 99.2%; Pred. No. 3.5e-66;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

```
Db      1  ARLETVTLGNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALKKRTVSVSQPSNRK 60
QY      61  NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRTETLAALLASPL 120
Db      61  NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRTETLAALLASPL 120
QY      121  LIDAIIDQLNPAY 132
Db      121  LIDAIIDQLNPAY 132
```

RESULT 15

```
US-10-050-902-258
; Sequence 258, Application US/10050302
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.019004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 258
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 259
; US-10-050-902-258
```

```
Query Match      99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  AKLEVTTLGNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALKKRTVSVSQPSNRK 60
Db      1  ARLETVTLGNIGDGRQTLVLPNGVPTNGVASLSQAGAVPALKKRTVSVSQPSNRK 60
QY      61  NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRTETLAALLASPL 120
Db      61  NYKVQVKIQNPPTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRTETLAALLASPL 120
QY      121  LIDAIIDQLNPAY 132
Db      121  LIDAIIDQLNPAY 132
```

Search completed: January 4, 2005, 09:41:23
Job time : 33.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 : Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-9

Perfect score: 664
Sequence: 1 AKLEVTTLGNIGDKGRQTLV.....ALLASPLLDALDQLNPAV 132

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	98.6	132	1	VCBPOB coat protein - pha
2	531.5	80.0	331	2	S01964 readthrough protei
3	116	17.5	131	1	VCBPP1 coat protein - pha
4	89.5	13.5	530	2	S22340 seeligertolysin -
5	85.5	12.9	540	2	T00646 hypothetical prote
6	84.5	12.7	529	2	S24231 listeriolysin O pr
7	84.5	12.7	529	2	A43505 listeriolysin O pr
8	84.5	12.7	529	2	AC1100 listeriolysin O pr
9	80.5	12.1	528	2	S22341 lysozyme precursor
10	80.5	12.1	1502	1	RGBYH1 CYC1/CYP3 transcr
11	79	11.9	282	2	A10186 probable iron-side
12	79	11.9	432	2	T31660 hypothetical prote
13	78	11.7	830	2	S5757 MT11 protein - yea
14	76.5	11.5	136	2	C98221 conserved hypochet
15	76.5	11.5	136	2	AE3065 conserved hypochet
16	76.5	11.5	1052	2	C64221 hypothetical 114k
17	76.5	11.5	1861	2	T13845 microtubule-assoc
18	75.5	11.4	1097	2	AD2572 hypothetical prote
19	75	11.3	130	1	AA6324 coat protein - pha
20	75	11.3	130	1	VCBPP1 coat protein - pha
21	74.5	11.2	161	4	I55480 coat protein - pha
22	74.5	11.2	130	1	VCBPP1 coat protein - pha
23	74	11.1	340	2	S18650 homeotic protein H
24	74	11.1	340	2	A42008 homeotic protein H
25	73.5	11.1	191	2	H90078 hypothetical prote
26	73.5	11.1	520	1	ACMSD1 nicotinic acetylch
27	73.5	11.1	601	2	A55921 serine/threonine k
28	73.5	11.1	719	2	T39271 conserved hypochet
29	73	11.0	430	2	G88884 protein K09B11.10

30	72.5	10.9	129	1	VCBPP2 coat protein - pha
31	72.5	10.9	129	1	VCBPP7 coat protein - pha
32	72.5	10.9	129	1	VCBPP7 coat protein - pha
33	72.5	10.9	289	2	C70400 ferredoxin oxidore
34	72	10.8	376	2	C84316 hypothetical prote
35	71.5	10.8	384	2	CA5490 neuropeptide Y/pep
36	71.5	10.8	458	2	T49114 hypothetical prote
37	71.5	10.8	654	2	S69673 SAC7 protein - yea
38	71	10.7	248	2	A86786 conserved hypochet
39	71	10.7	366	2	F70618 probable pntA pro
40	71	10.7	399	1	A43685 polymerase-associ
41	71	10.7	434	2	S72430 transcription elon
42	71	10.7	434	2	D88305 protein R03D7.4 [l
43	71	10.7	463	2	S00676 translational elonga
44	71	10.7	1461	2	E90696 hypothetical prote
45	71	10.7	1461	2	A85547 hypothetical prote

ALIGNMENTS

RESULT 1

VCBPOB coat protein - phase Q-beta

C/Species: phage Q-beta

C/Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004

C/Accession: A92240; A92221; A92088; A04224

R/Bscarmis, C.; Saccary, P.A.; Billeter, M.A.

J. Biol. Chem. 253, 8390-8399, 1978

A/Title: Determination of the first half of the coat protein cistron of bacteriophage Qb

A/Reference number: A92240; PMID:79048469; PMID:361741

A/Accession: A92240

A/Molecule type: mRNA

A/Residues: 1-80 <ESC>

A/Cross-references: UNIPROT:P03615

J. Biol. Chem. 252, 990-993, 1977

J. Biol. Chem. 252, 990-993, 1977

A/Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.

A/Reference number: A92221; PMID:77118576; PMID:838709

A/Accession: A92221

A/Molecule type: protein

A/Residues: 1-60 <STO>

R/Malta, T.; Konigsberg, W.

J. Biol. Chem. 246, 5003-5024, 1971

A/Title: The amino acid sequence of the Qbeta coat protein.

A/Reference number: A92088; PMID:7128580; PMID:5570434

A/Accession: A92088

A/Molecule type: protein

A/Residues: 1-21, 'D', '23-55', '132' <MAI>

C/Superfamily: phage GA coat protein

Query Match 98.6%; Score 655; DB 1; Length 132;

Best Local Similarity 98.5%; Pred. No. 1e-56; Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	AKLEVTTLGNIGDKGRQTLVNPRTNGVSLSOAGVPALEKRVTVSOPSNNRK	60
DB	1	AKLEVTTLGNIGDKGRQTLVNPRTNGVSLSOAGVPALEKRVTVSOPSNNRK	60
QY	61	NYKVQKIQNPACTANGSCDPSVTRQKADVTFSFYQSTDEBRAVFTLALASPL	120
DB	61	NYKVQKIQNPACTANGSCDPSVTRQKADVTFSFYQSTDEBRAVFTLALASPL	120
QY	121	LIDALDQLNPAV 132	
DB	121	LIDALDQLNPAV 132	

RESULT 2

S01964 readthrough protein - phase SP

C/Species: phage SP

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S01964
C:Inokuchi, Y.; Jacobson, A.B.; Hirose, T.; Inayama, S.; Hirashima, A.
Nucleic Acids Res. 16, 6205-6221, 1988
A:Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP
A:Reference number: S01963; MUID:88289362; PMID:3399390
A:Accession: S01964
A:Status: preliminary
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-331 <INO>
A:Cross-references: UNIPROT:P09677; EMBL:X07489
A:Note: the authors translated the readthrough stopcodon TGA for residue 133 as Tyr
A:Superfamily: phage GA coat protein

Query Match	80.0%	Score 531.5	DB 2	Length 331
Best Local Similarity	78.8%	Pred. No. 3.3e-44		
Matches 104	Conservative 12	Mismatches 15	Indels 1	Gaps 1

```
QY      1 AKLEVTYTLGNIGKDGQRTVLNPRGVNPTNGVASLSQAGAVPALEKRYTVSVSPSRNK 60
      ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2 AKLNQYTLISKGKNGDQTLTLPRGVNPTNGVASLSSEAGAVPALEKRYTVSVAPSRNK 61
```

```
QY      61 NYKQVQKIQNPACTANGSCDPSVTQKYADVTFSFQYQSIDEEARVRTTEALALLSPL 120
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      62 NFKVQIKLQNPACTARD-ACDPSVTSFAFADVTLSFTSYSTDEBRALRTTEALALLDPL 120
```

Qy	121	LIDAIQNLNPA	132
		::: : : : :	
Db	121	IVDAIDNLNPA	132

RESULT 3
VCBPPI

coat protein - phage PRR1
C:Species: phage PRR1
C:Date: 30-Nov-1979 #sequence_ revision 30-Nov-1979 #text_change 09-Jul-2004

C/Accession: A04225
R;Dhaese, P.; Vandekerckhove, J.S.; Van Montagu, M.C.
Eur. J. Biochem. 84 375-385 1979

Eur. J. Biochem. 94, 375-386, 1979
 A1>Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage phi29
 A1:Reference number: A04225; MUID:79148387; PMID:107028
 A1:Accession: 204225

A: Molecule type: protein
A: Residues: 1-131 <DHA>
A: Cross-references: UNIPROT:P03616
C: Superfamily: phage GA coat protein

Query Match	17.5%;	Score 116;	DB 1;	Length 131;
Best Local Similarity	32.3%;	Pred. No. 0.00038;		
Matches 42;	Conservative 14;	Mismatches 58;	Indels	

0y 17 QTLVILNPRCAVPT-----NGVASLSQAGAVPALERVTYVSQSPBRNRKNKYGV 66
 4 QNLYLKREATPNHPTFVPDIDIRNVGEVESTGVPIGSEFTLSLRKTSNGR--YKSTL 61
 Db

QY 67 KIQNPT-ACTANGSCDSPVTRÖKADVTFSFTÖYSTDEER-AFVRTEIAALIASPLLI- 122
| : | : | : | : | : | : | : | : | : | :
Db 62 KLAVPEVQSÖTVNGIIVTPVVVRTSYTVDPEFDARSTTKERRNPFVGMTADALKADMVH 122

QY	123 DAIDQNPAY	132
Db	122 DTIVNLQGVY	131

RESULT 4

S22340
seeligeriolysin - *Listeria seeligeri*

```
Cispecies: Listeria seeligeri
CIdate: 22-Nov-1993 #sequence_01-Dec-1995 #ext_change_09-Jul-2004
CAccession: S22340
```

R;Haas, A.; Dumbsky, M.; Krefc, J.
Biochim. Biophys. Acta 1130: 81-84, 1992.
C/Accession: S22340

A/Title: *Listerioidysin* genes: complete sequence of *llo* from *Listeria Ivanovi* and of *lsc*

A:Accession: S22340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <HAA>
A:Cross-references: UNIPROT:P31830; EMBL:X60462; NID:944144; PIRN:CAA42996.1; PTD:944145
A>Note: the authors translated the codon GCC for residue 287 as Pro
C:Superfamily: dipeptide transport protein

Query Match	13.5%	Score	89.5	DB	2	Length	530
Best Local Similarity	25.0%	Pred. No.	0.73				
Matches	34	Conservative	22	Mismatches	37	Indels	43
						Gaps	7

QY 13 KDRGQIVL--NRGVNPT-----NCVASLSQAG-----VPALKERV 48
Db 94 KDSEYIVAEKKKGINONNADISVINISSLTPGALVKANRELVENQNVTPVVKDSL 153

```
Qy      49 TVSVSQPSNRKKNYKVQKIQNPCTANGSCDPVTR--QKY-----ADVTFSFTQ  98
      ||| : : : ||| : : : ||| : : :
Db      154 TLSVDLPGMTKKDKNKIFVK--NPPTSNVANNVTLVERMDKYSKALPNINAKIDYS--- 208
```

QY 99 YSTDEERAFVTELAA 114
: | | : : | |
Db 209 ---DEMAYSESOLIA 220

RESULT 5
T00646

C:Accession: T00646
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Provenance: Provenance: Italy, in the Alps, near Innsbruck, Austria

R.Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo, Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologos, A.; Davis, R.W.
submitted to the EMBL Data Library, February 1998

A;Reference number: Z14197

A:Accession: T00646
A:Status: translated from GB/EMBL/DBJ

A: Molecule type: DNA
A: Residues: 1-540 <FED>
A: Cross-references: UNIPROT:O48683; EMBL:AC002396; NID:g274918; PIDD:AA00577.1; PID:g28

C:Genetics:
A:Gene: ATSP.F316.9
A:Map position: 1
A:introns: 14/3, 281/3, 428/3, 448/2, 483/3, 502/3
C:Superfamily: pyruvate dehydrogenase (lipoamide)

Query Match	12.9%	Score 85.5;	DB 2;	Length 540;
Best Local Similarity	26.1%	Pred. No. 1.8;		
Matches 30;	Conservative 15;	Mismatches 55;	Indels 15;	Gaps 3;

```

09      11 IGDGRQTLVLNPRG---VNPPTNGVASLSQAGAVPALEKRYTVSVSQPSRRNKN-YKQV 66
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db     255 VKKEKKPNLIKQDGNVRINPTRSLKPNQVGKPEPTNKTYTSRKRPSPSKEMKNMMKATK 314

```

```

Qy      67 KIQNPACTANGSCDPSTVRQKVADVTFSPQYSTDEERAFVRELAALASPLL 121
        | : : | : : : : : : : : : : : : : : : : : : : : :
Db      315 KPAAPMSKSPQGFATPRVYKPPAPITSLSTSHSLKKEK-----VSPLL 358

```

RESULT 6
S24231

A;Variet

C:\Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:\Accession: S24231

R; Rasmussen, O. F.; Beck, T.; Olsen, J. E.; Dons, L.; Rossen, L. Infect. Immun. 59, 3945-3951, 1991

A;Title: Bacteria monocytogenes isolates can be classified
A;Reference number: S24230; MUID:92040062; PMID:19377533
A;Accession: S24231

A/Accession: S44251
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A;Residues: 1-529 <RAS>
A;Cross-references: UNIPROT:P13128; EMBL:X60035; NID:G44110; PIDN:CAA42639.1; PID:G44112
A;Experimental source: strain 12067, serotype 4b
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C;Genetics:
A;Gene: 116A
C;Superfamily: dipeptide transport protein
C;Keywords: virulence factor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-529/Product: listeriolysin #status predicted <MAT>
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
Qy 13 KQGRQTLV-----NPRGVNPTNGVASLSQAG-----VPALEKRV 48
Db 93 KQGENEYIVAEKKKKSINQNNADIQVNAISLTPGALVKANSELVENQPDVLPVKRDSL 152
Qy 49 TVSVSQPSNRKRYKQVQKIQNPACTANGSCDPSVTR-----QKYADVTSFTQYSTD 102
Db 153 TTSIDLPGMTNQDNKIVK--NATKSNVNNVAVTLVERNMEKKAQAYPNVS---AKIDYD 207
Qy 103 EERAFVRTIELAA 114
Db 208 DEMAYSESQILIA 219
RESULT 7
A43505
Listeriolysin O precursor - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C;Accession: A43505; S05306; A47606; S12400; A61079
R;Mengaud, J.; Vicens, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanzey
Infect. Immun. 56, 766-772, 1988
A;Title: Expression in *Escherichia coli* and sequence analysis of the listeriolysin O det
A;Reference number: A43505; MUID:88153053; PMID:3126142
A;Accession: A43505
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <MEN>
A;Cross-references: UNIPROT:P13128; GB:M24199; NID:G149652; PIDN:AAA03018.1; PID:G149653
A;Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R;Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A;Title: Nucleotide sequence of the listeriolysin gene from a *Listeria monocytogenes* ser
A;Reference number: S05306; MUID:89366684; PMID:2505236
A;Accession: S05306
A;Molecule type: DNA
A;Residues: 1-529 <DOM>
A;Cross-references: EMBL:X15127; NID:G44106; PIDN:CAA33223.1; PID:G44107
A;Experimental source: strain EGD
A;Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R;Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cossart, P.
Infect. Immun. 55, 3225-3227, 1987
A;Title: Identification of the structural gene encoding the SH-activated hemolysin of *Li*
A;Reference number: A47606; MUID:88057627; PMID:2824384
A;Accession: A47606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 413-480 <ME2>
A;Cross-references: GB:M29171
R;Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A;Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtain
A;Reference number: S12400; MUID:91211627; PMID:1965218
A;Accession: S12400
A;Molecule type: DNA
A;Residues: 483-493 <MIC>
A;Experimental source: strain LO28, serotype 1/2c
C;Genetics:
A;Gene: hlyA; 116A

C;Superfamily: dipeptide transport protein
C;Keywords: virulence factor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-529/Product: listeriolysin O #status predicted <MAT>
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
Qy 13 KQGRQTLV-----NPRGVNPTNGVASLSQAG-----VPALEKRV 48
Db 93 KQGENEYIVAEKKKKSINQNNADIQVNAISLTPGALVKANSELVENQPDVLPVKRDSL 152
Qy 49 TVSVSQPSNRKRYKQVQKIQNPACTANGSCDPSVTR-----QKYADVTSFTQYSTD 102
Db 153 TTSIDLPGMTNQDNKIVK--NATKSNVNNVAVTLVERNMEKKAQAYPNVS---AKIDYD 207
Qy 103 EERAFVRTIELAA 114
Db 208 DEMAYSESQILIA 219
RESULT 8
AC1100
Listeriolysin O precursor [imported] - *Listeria monocytogenes* (strain EGD-e)
C;Species: *Listeria monocytogenes*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1100
R;Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauger, O.; Entian, K.D.; Feihl, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maltournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tjerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species
A;Reference number: AB1077; MUID:2157279; PMID:11679669
A;Accession: AC1100
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <GLA>
A;Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:G16409567; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: hlyA
C;Superfamily: dipeptide transport protein
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
Qy 13 KQGRQTLV-----NPRGVNPTNGVASLSQAG-----VPALEKRV 48
Db 93 KQGENEYIVAEKKKKSINQNNADIQVNAISLTPGALVKANSELVENQPDVLPVKRDSL 152
Qy 49 TVSVSQPSNRKRYKQVQKIQNPACTANGSCDPSVTR-----QKYADVTSFTQYSTD 102
Db 153 TTSIDLPGMTNQDNKIVK--NATKSNVNNVAVTLVERNMEKKAQAYPNVS---AKIDYD 207
Qy 103 EERAFVRTIELAA 114
Db 208 DEMAYSESQILIA 219
RESULT 9
S22341
Listeriolysin precursor - *Listeria ivanovii*
C;Species: *Listeria ivanovii*
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S22341; S36683
R;Haas, A.; Dumbeky, M.; Kreft, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A;Title: Listeriolysin genes: complete sequence of 110 from *Listeria ivanovii* and of 180
A;Reference number: S22340; MUID:92182018; PMID:1543752

A/Accession: S22341
 A/Molecule type: DNA
 A/Residues: 1-528 <HAS>
 A/Cross-references: UNIPROT:P31831; EMBL:X60461
 A/Note: the authors translated the codon ACA for residue 331 as Val
 R/Kreff, J.
 Submitted to the EMBL Data Library, July 1991
 A/Reference number: S36683
 A/Accession: S36683
 A/Molecule type: DNA
 A/Residues: 1-319, 'T', 321-528 <KRB>
 A/Cross-references: EMBL:X60461
 C/Genetics:
 A/Gene: 110
 C/Superfamily: dipeptide transport protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-528/Product: vanolysin #status predicted <MA>

Query Match 12.1%; Score 80.5; DB 2; Length 528;
 Best Local Similarity 22.0%; Pred. No. 5.5;
 Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGROTLVLP-----NRGVNPTNGVSLSGAG-----VPALEKRY 48
 Db 92 KEGNQYIVVERKKKKKINONNADIQVINSLSLTYPGALVKANSELVENOPDVLVPRDSV 151
 QY 49 TVGVSCPSRRNRKRYVKVQKIQNPACTANGSCDPSVTR-----QRYADVTFSTGYSTD 102
 Db 152 TLISIDLP--GMVHNDNIIVVQNAITKSNINGVMTLVDRMNNKXSEEPNIS---AKIDVD 206
 QY 103 EERAFVTEIAA 114
 Db 207 QEMAYSESQIVA 218

RESULT 10

RGBYH1
 CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
 N/Alternate names: protein L9672.1; protein YLR256w; regulatory protein CYP1; regulatory
 C/Species: Saccharomyces cerevisiae
 C/Date: 30-Sep-1991 #sequence revision 23-Feb-1996 #text_change 12-Nov-1999
 C/Accession: S59400; A31312; S15447; S05804; S15446
 R/Johnson, D.
 Submitted to the EMBL Data Library, February 1995
 A/Description: The sequence of S. cerevisiae cosmid 9672.
 A/Reference number: S59386
 A/Accession: S59400
 A/Molecule type: DNA
 A/Residues: 1-1502 <JOH>
 A/Cross-references: EMBL:U20865; NID:G662330; PIDN:AB67387.1; PID:G662331; GSPDB:GN0001
 A/Experimental source: strain S288C (AB972)
 R/Pfeffer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
 Cell 56, 291-301, 1989

A/Title: Functional dissection and sequence of yeast HAP1 activator.
 A/Reference number: A31312; MUID:89106221; PMID:2643482
 A/Accession: A31312
 A/Molecule type: DNA
 A/Residues: 1-144, 'I', 146-322, 'R', 324-454, 'N', 456-507, 'M', 509-586, 'K', 588-882, 'N', 884-95
 A/Cross-references: EMBL:J03152; NID:G171645; PIDN:AAA34662.1; PID:G171646
 R/Crennot, F.; Verdier, J.; Gaisne, M.; Slonimski, P.P.
 J. Mol. Biol. 204, 263-276, 1988
 A/Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
 A/Reference number: S15447; MUID:89125585; PMID:2851658
 A/Accession: S15447
 A/Molecule type: DNA
 A/Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADPFIW' <CREI>
 A/Note: the sequence is from mutant CYP1-18
 A/Cross-references: EMBL:X13793
 C/Genetics:
 A/Gene: SGD:HAP1, CYP1; MIPS:YLR256w
 A/Cross-references: SGD:S0004246; MIPS:YLR256w
 A/Map position: 12R
 C/Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology

C/Keywords: DNA binding; heme binding; transcription regulation; zinc finger
 F:1-148/Domain: DNA binding #status predicted <DNA>
 F:159-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F:64-84/Region: zinc finger CCCC motif
 F:177-189/Region: glutamine-rich
 F:245-445/Domain: heme binding #status predicted <HEM>
 F:299-304, 323-328, 347-352, 373-378, 389-394, 415-420/Region: 6-residue repeats
 F:1308-1481/Domain: activation element #status predicted <ACT>
 F:1388-1481/Region: acidic

Query Match 12.1%; Score 80.5; DB 1; Length 1502;
 Best Local Similarity 20.6%; Pred. No. 18;
 Matches 35; Conservative 30; Mismatches 42; Indels 63; Gaps 7;

QY 23 PRGVN--PTNGVSL-----SQAGVPALEKRYTVSVS 53
 Db 1278 PRGISRKPNSGLSSVPLSSFSMNQNGTIPVSLNITSQMALSLSDITTNQIN 1337
 QY 54 QPSRRN-KRYKVKVQKIQNP-----TACTANGSCP 82
 Db 1338 LPDPSRDEAFDINSIKQMTPTSAFNNANTTIPSTLNGMNMNGAGTAATDTSANGSALS 1397
 QY 83 SVYRQKXADV-TFSFQYSTD--EERAFVTEIAALASP-LLIDALDQAN 129
 Db 1398 TLITSPQSDIASNSATQYKPDLEDPLMNSNFMNPSLVEVGGYN 1447

RESULT 11

A10186
 Probable iron-siderophore transport system, ATP-binding component YPO1533 [imported] - Ye
 C/Species: Yersinia pestis
 C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C/Accession: A10186
 R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 demo-tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
 Nature 413, 523-527, 2001
 A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A/Reference number: AB0001; MUID:21470413; PMID:11586360
 A/Accession: A10186
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-282 <KUR>
 A/Cross-references: UNIPROT:Q8ZF20; GB:AL590842; PIDN:CAC90356.1; PID:G15979576; GSPDB:GT
 C/Genetics:
 A/Gene: YPO1533
 C/Superfamily: inner membrane protein malK; ATP-binding cassette homology

Query Match 11.9%; Score 79; DB 2; Length 282;
 Best Local Similarity 22.0%; Pred. No. 3.7;
 Matches 27; Conservative 37; Mismatches 45; Indels 14; Gaps 5;

QY 13 KDGROTLVNPMPNPTNGVSLSGAGVPALEKRYTVSVSPSRNRKRYKVKQKQNP 72
 Db 49 KNGAFSVITIGPNCCKSTLLRALSR-----LIPQNSIRLQ--QIQYKAKVPAKQUS 102
 QY 73 ACTANGSCPVSAT-----RQKXADVTFSTGYSTDEERAFVTEIAALASPLLIDAID 126
 Db 103 LLSQGSASISSETITLTPDLVSRGYAHQSF-FHQWSTEDER-IYKAISAVNLSIVGQRVS 160
 QY 127 QAN 129
 Db 161 ELS 163

RESULT 12

T31660
 Hypothetical protein COS41.6 - sea squirt (Cliona intestinalis)
 C/Species: Cliona intestinalis
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T31660
 R/Bird, A.P.; Clark, V.; Jones, S.J.; Leitzgeb, S.; Dobson, R.; Tweedle, S.
 Submitted to the EMBL Data Library, December 1996

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-9

Perfect score: 664
Sequence: 1 AKLEVTYIGNIKGRQTLV.....AALASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_02:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	98.6	132	1	COAT_BPOBE
2	655	98.6	133	2	AAM3126 bacterioph
3	655	98.6	329	2	O81T61 bacterioph
4	655	98.6	329	2	AAL1663 bacterioph
5	566	85.2	133	2	O9T0R9 enterobacte
6	566	85.2	329	2	O64307 enterobacte
7	546	82.2	133	2	O9T0S0 bacterioph
8	546	82.2	329	2	O64303 bacterioph
9	531.5	80.0	132	1	COAT_BPSP
10	531.5	80.0	331	1	VAL_BPSP
11	499.5	75.2	132	2	O9T0R8 enterobacte
12	499.5	75.2	330	2	O64310 enterobacte
13	116	17.5	131	1	COAT_BPPRR
14	96.5	14.5	473	2	O8VDC2 mus muscula
15	89.5	13.5	530	1	TACY_LISSE
16	89.5	13.5	530	2	AAP97361 listeria
17	85.5	12.9	540	2	O48683 arabidopsi
18	84.5	12.7	529	1	TACY_LISMF
19	84.5	12.7	529	1	TACY_LISMO
20	84.5	12.7	529	2	O9L5B9 listeria mo
21	84.5	12.7	529	2	O6E942 listeria mo
22	84.5	12.7	529	2	O6E9A2 listeria mo
23	84.5	12.7	529	2	O6E9G2 listeria mo
24	84.5	12.7	529	2	O6E9Q2 listeria mo
25	84.5	12.7	529	2	O6E9T2 listeria mo
26	84.5	12.7	529	2	O6E9A28 listeria mo
27	84.5	12.7	529	2	O6E9A6 listeria mo
28	84.5	12.7	529	2	O6E9A7 listeria mo
29	84.5	12.7	529	2	O6E9A0 listeria mo
30	84.5	12.7	529	2	O6E9A4 listeria mo
31	84.5	12.7	529	2	AAT03000 listeria

32	82	12.3	1624	2	O9V3K8	O9V3K8 drosophila
33	82	12.3	1637	2	O95KR8	O95KR8 drosophila
34	81	12.2	336	2	O8TRF3	O8TRF3 methanosa
35	80.5	12.1	528	1	TACY_LISIV	P31631 listeria iv
36	80.5	12.1	528	2	O6R6D9	O6R6D9 listeria iv
37	80.5	12.1	528	2	AAR97343	AAR97343 listeria
38	80.5	12.1	1502	1	CYPI_YEAST	P12351 baccharomyc
39	79.5	12.0	608	2	O84H79	O84H79 rhodococcus
40	79	11.9	282	2	O8ZEZ0	O8ZEZ0 yersinia pe
41	79	11.9	282	2	AAS61663	AAS61663 yersinia
42	79	11.9	325	2	O73R79	O73R79 treponema d
43	79	11.9	325	2	AAS10709	AAS10709 treponema
44	79	11.9	432	2	P91584	P91584 ciona intes
45	79	11.9	512	2	O6HGA7	O6HGA7 bacillus th

ALIGNMENTS

RESULT 1
COAT_BPOBE STANDARD; PRT; 132 AA.
ID COAT_BPOBE
AC P036T5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clemons I., Drellina D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137,133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarot C., Sastre P.A., Biller M.A.;
RT "Determination of the first half of the coat protein cistron of
RT bacteriophage Q-beta as an application of a mapping procedure for RNA
RT fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Scoll B., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
RT and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maite T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundale M., Valgard K., Liljas L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
CC -!- FUNCTION: Forms the phage shell, binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: M99039; AAA16662.1; -.
DR EMBL: V00643; CAA23992.1; -.
DR PIR: A92240; VCBPOB.
DR PDB: 1QBE; X-ray; A/B/C=1-132.
DR InterPro: IPR002703; Levi coat.
DR Pfam: PF01819; Levi coat; 1.
KM 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
FT INIT MET 0 0
FT 22 22 N -> D (in Ref. 4).
FT CONFLICT 56 56 Missing (in Ref. 4).
FT STRAND 6 9
FT TURN 13 14
FT STRAND 18 27
FT TURN 28 31
FT STRAND 32 36
FT HELIX 42 44
FT STRAND 47 53
FT STRAND 56 56
FT TURN 57 58
FT STRAND 59 59
FT STRAND 62 74
FT STRAND 83 96
FT TURN 98 99
FT HELIX 102 117
FT HELIX 119 126
FT TURN 127 127
SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 98.6%; Score 655; DB 1; Length 132;
Best Local Similarity 98.5%; Pred. No. 1.7e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
DB 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALIASPL 120
DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALIASPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 2
AA33126 PRELIMINARY; PRT; 133 AA.
ID AAM3126
AC AAM3126;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses; Alloviridae subgroups III.
OX NCBI_Taxid=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
DR EMBL: AY099114; AAM3126.1; -.
KW Coat protein.
SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.6%; Score 655; DB 2; Length 133;
Best Local Similarity 98.5%; Pred. No. 1.7e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
DB 2 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALIASPL 121
QY 121 LIDAIDQLNPAY 132
DB 122 LIDAIDQLNPAY 133

RESULT 3
O8LTEL
ID O8LTEL PRELIMINARY; PRT; 329 AA.
AC O8LTEL;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE A1 read-through protein (A1 protein).
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviruses.
OX NCBI_Taxid=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Chelens I., Dreilina D., Dislers A., Baumanns V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-assembled in Escherichia coli."
RL Gene 137:133-137(1993).
DR EMBL: M99039; AAA16663.1; -.
DR EMBL: M99039; AAA16663.1; -.
DR HSSP: P03615; 1QBE.
DR GO: GO:0019026; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002703; Levi coat.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF01819; Levi_coat_1.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.6%; Score 655; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 4.8e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 60
DB 2 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALIASPL 121
QY 121 LIDAIDQLNPAY 132
DB 122 LIDAIDQLNPAY 133

RESULT 4
AAA16663
ID AAA16663 PRELIMINARY; PRT; 329 AA.
AC AAA16663;
DT 02-MAR-2004 (TReMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DE 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
NCBI Taxid=12009;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clemons I., Dreilima D., Dislers A., Baumanie V.,
Ose V., Pumpens P.,
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli."
RL Gene 137.133-137(1993).
DR EMBL, M99039; AAA16663.1; -
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.6%; Score 655; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 4.8e-55;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 60
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DE 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
NCBI Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., Poot R., van Duin J.,
RT "Secondary structure model for the first three domains of single-stranded
RT RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.,
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF059242; AAC14699.1; -
DR HSSP, P03615; IOBE.
DR GO, GO:0019028; C:Viral capsid; IEA.
DR GO, GO:0005198; F:Structural molecule activity; IEA.
DR InterPro, IPR002703; Lev1_coat.
DR Pfam, PF01819; Lev1_coat; 1.
KW Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;
RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
AC Q9TOR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
NCBI Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.,
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF059242; AAC14700.1; -
DR HSSP, P03615; IOBE.
DR GO, GO:0019028; C:Viral capsid; IEA.
DR GO, GO:0005198; F:Structural molecule activity; IEA.
DR InterPro, IPR002703; Lev1_coat.
DR Pfam, PF01819; Lev1_coat; 1.
DR PROSITE, PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 85.2%; Score 566; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 2e-46;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 60
DB 2 AKLOATTLTSGIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALADPM 121
QY 121 LIDAIDLNLPAY 132
DB 122 LIDAIDLNLPAY 133
RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
NCBI Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.,
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF059242; AAC14700.1; -
DR HSSP, P03615; IOBE.
DR GO, GO:0019028; C:Viral capsid; IEA.
DR GO, GO:0005198; F:Structural molecule activity; IEA.
DR InterPro, IPR002703; Lev1_coat.
DR Pfam, PF01819; Lev1_coat; 1.
DR PROSITE, PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 85.2%; Score 566; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 2e-46;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 60
DB 2 AKLOATTLTSGIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALADPM 121
QY 121 LIDAIDLNLPAY 132
DB 122 LIDAIDLNLPAY 133

Query Match 85.2%; Score 566; DB 2; Length 133;
Best Local Similarity 83.3%; Pred. No. 7.1e-47;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 60
DB 2 AKLOATTLTSGIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALADPM 121
QY 121 LIDAIDLNLPAY 132
DB 122 LIDAIDLNLPAY 133
RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
NCBI Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.,
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF059242; AAC14700.1; -
DR HSSP, P03615; IOBE.
DR GO, GO:0019028; C:Viral capsid; IEA.
DR GO, GO:0005198; F:Structural molecule activity; IEA.
DR InterPro, IPR002703; Lev1_coat.
DR Pfam, PF01819; Lev1_coat; 1.
DR PROSITE, PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 85.2%; Score 566; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 2e-46;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 60
DB 2 AKLOATTLTSGIGKDGQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNRK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRETELAAALADPM 121
QY 121 LIDAIDLNLPAY 132
DB 122 LIDAIDLNLPAY 133

Query	Subject	Score	Length	Mismatches	Conservative	Indels	Gaps
Q1	AKLETVTLGNIGKGRQTLVINPRGVNPTNGVASISQGANVPALAEKRYTVSVSGPSRRNK	60	133	0	106	12	0
Q2	AKLQAVITLSGIGKKGVDVTLIDNPRGVNPTNGVAAALSEAGAVPALEKRYTVISVSGPSRRNK	61	133	0	106	12	0
Q3	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	120	133	0	106	12	0
Q4	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	121	133	0	106	12	0
Q5	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	122	133	0	106	12	0
Q6	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	123	133	0	106	12	0
Q7	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	124	133	0	106	12	0
Q8	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	125	133	0	106	12	0
Q9	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	126	133	0	106	12	0
Q10	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	127	133	0	106	12	0
Q11	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	128	133	0	106	12	0
Q12	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	129	133	0	106	12	0
Q13	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	130	133	0	106	12	0
Q14	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	131	133	0	106	12	0
Q15	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	132	133	0	106	12	0
Q16	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	133	133	0	106	12	0
Q17	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	134	133	0	106	12	0
Q18	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	135	133	0	106	12	0
Q19	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	136	133	0	106	12	0
Q20	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	137	133	0	106	12	0
Q21	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	138	133	0	106	12	0
Q22	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	139	133	0	106	12	0
Q23	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	140	133	0	106	12	0
Q24	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	141	133	0	106	12	0
Q25	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	142	133	0	106	12	0
Q26	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	143	133	0	106	12	0
Q27	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	144	133	0	106	12	0
Q28	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	145	133	0	106	12	0
Q29	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	146	133	0	106	12	0
Q30	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	147	133	0	106	12	0
Q31	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	148	133	0	106	12	0
Q32	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	149	133	0	106	12	0
Q33	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	150	133	0	106	12	0
Q34	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	151	133	0	106	12	0
Q35	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	152	133	0	106	12	0
Q36	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	153	133	0	106	12	0
Q37	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	154	133	0	106	12	0
Q38	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	155	133	0	106	12	0
Q39	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	156	133	0	106	12	0
Q40	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	157	133	0	106	12	0
Q41	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	158	133	0	106	12	0
Q42	NYKQVQKIONFTACANGSCDPSVTRQKADVTSFTQYSDNDEBPVRYTEALALLLSPL	159	133	0	106	12	0

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.; ; single-stranded
RA "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF0522431; AAC06251.1; -.
DR HSSP; P019615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RM_RNP_1; UNKOWN 1.
SQ SEQUENCE 329 AA; 35693 MW; 3B33CD821EE625F4 CRC64;

Query Match          82.2%; Score 546; DB 2; Length 329;
Best Local Similarity 80.3%; Pred. No. 1.8e-44;
Matches 106; Conservative %12; Mismatches 14; Indels 0; Gaps 0;

QY      1 AKLEETWLTGNIGKHGRQTIVLNPGVNPPTNGVASLSQAGAVPALEKRVTVSVSPSRRK 60
Db       2 AKQCATILSGIGKKGDVTLIDNPGVNPPTGVAAISGAGVPALEKRVTVSVSPSRRK 61
QY      61 NYKVQVKIIONPIACTANGSCDPVSVTROKRVADVTFTSYSTDEBRFAVRTELALASPL 120
Db       62 NYKVQVKIQNPSTCTASGTCDDPSVTRSAVSDFTSFYQSVTERALVRTELQLADPM 121
QY      121 LIDAIDQINPAY 132
Db       122 LVNAIDMLNPAY 133

RESULT 9
COAT_BPSP STANDARD; PRT; 132 AA.
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
OX NCBI_TaxID=12027;
RN RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP."
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Forms the phage shell. binds to the phage RNA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; X07489; CA30374.1; -.
HSSP; P03615; IOBE.
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DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
DR Coat protein; RNA-binding.
SQ SEQUENCE 132 AA; 14128 MW; 50B1E6CC6AFOA254 CRC64;

Query Match 80.0%; Score 531.5; DB 1; Length 132;
Best Local Similarity 78.8%; Pred. No. 1.5e-43;
Matches 104; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLGQAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLNQVTLTKIGNGQTLTLTPRGVNPPTNGVSLGQAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NKVQVQIKQNPACTANGSCDPSVTRQKADVTFFSTQYSTDEBRARFVTELAALIASPL 120
DB 62 NKVQVQIKQNPACTANGSCDPSVTRQKADVTFFSTQYSTDEBRARFVTELAALIASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 10
VAL_BPSP STANDARD; PRT; 331 AA.
AC P09677;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Reatthrough protein A1 [contains: Coat protein].
OS Bacteriophage SP.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolievirus.
OX NCBI_Taxid=12077;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirschman A., Hirose T., Inakuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
coliphage SP.".
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The reatthrough protein A1 includes the coat
protein sequence.

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CC
CC EMBL; X07489; CAB37299.1; -.
DR PIR; S01964; S01964.
DR HSSP; P03615; 10BE.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KM Coat protein.
FT CHAIN 1 132 Coat protein.
FT CHAIN 1 331 Reatthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A664284B52C6582 CRC64;

Query Match 80.0%; Score 531.5; DB 1; Length 331;
Best Local Similarity 78.8%; Pred. No. 4.5e-43;
Matches 104; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLGQAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLNQVTLTKIGNGQTLTLTPRGVNPPTNGVSLGQAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NKVQVQIKQNPACTANGSCDPSVTRQKADVTFFSTQYSTDEBRARFVTELAALIASPL 120
DB 121 IYDAIDNINPAY 132

DB 62 NKVQVQIKQNPACTANGSCDPSVTRQKADVTFFSTQYSTDEBRARFVTELAALIASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 11
Q9TOR8 PRELIMINARY; PRT; 132 AA.
ID Q9TOR8
AC Q9TOR8;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NL95.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolievirus.
OX NCBI_Taxid=75725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.".
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Root R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.".
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059243; AAC14703.1; -.
DR HSSP; P03615; 10BE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KM Coat protein.
SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 75.2%; Score 499.5; DB 2; Length 132;
Best Local Similarity 75.8%; Pred. No. 1.9e-40;
Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 AKLEVTTLGNIGKDGQTLVLPNGVNPPTNGVSLGQAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLNQVTLTKIGNGQTLTLTPRGVNPPTNGVSLGQAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NKVQVQIKQNPACTANGSCDPSVTRQKADVTFFSTQYSTDEBRARFVTELAALIASPL 120
DB 62 NKVQVQIKQNPACTANGSCDPSVTRQKADVTFFSTQYSTDEBRARFVTELAALIASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 12
O64310 PRELIMINARY; PRT; 330 AA.
ID O64310
AC O64310;
DT 01-AUG-1998 (TREMELrel. 07, Created)
DT 01-AUG-1998 (TREMELrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage NL95.
OC Viruses; sRNA positive-strand viruses, no DNA stage; Leviviridae;

OC Allotetivirus.
 OX NCBI_TaxID=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta."
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis."
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF059243; AAC14704.1; -.
 DR HSSP: P03615; 108; C:Viral capsid; IEA.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR002703; Levi coat.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF01819; Levi coat; 1.
 DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 330 AA; 36175 MW; 961B55F408334410 CRC64;
 Query Match 75.4%; Score 499.5; DB 2; Length 330;
 Best Local Similarity 75.8%; Pred. No. 5.6e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKETVTLGNIGDGRQTLVLRGVNPTNGVSLSGAGVPALEKRYTVSVQPSNRK 60
 DB 2 AKNKVTTLTGIGAGNQTLTLTRGVNPTNGVSLSGAGVPALEKRYTVSVQPSNRK 61
 QY 61 NYKQVQKIQNPACTANGSCDPSVTROKVDYTFSPQYSTDEERAFVTELAALASPL 120
 DB 62 NYKQVQKIQNPACTANGSCDPSVTROKVDYTFSPQYSTDEERAFVTELAALASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 IYDAIDQLNPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR STANDARD; PRT; 131 AA.
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PRR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OX NCBI_TaxID=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhaese P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PRR1."
 RL Eur. J. Biochem. 94:375-386(1979).
 CC - FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR InterPro: IPR002703; Levi coat.
 DR Pfam: PF01819; Levi coat; 1.
 KM Coat protein; direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7B59E1E50FC612 CRC64;

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0028;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTVLNPGRVNP-----NGVASLSQAGVPALEKRYTVSVQPSNRKRYKQV 66
 DB 4 QNVLVDRATPDHTFVRPRDIRDNGEVEESGVIGSRFTISLRKTSNGR--YKSTL 61
 QY 67 KIQNPT--ACTANGSCDPSVTROKVDYTFSPQYSTDEERAFVTELAALASPLLI- 122
 DB 62 KLVVPVQSGTVNGIYTPVAVRTSYTVPDIDARSTTERNNFVGMIDALKADMLVH 121
 QY 123 DAIDQLNPAY 132
 DB 122 DTVNQLGVY 131
 RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2 PRELIMINARY; PRT; 473 AA.
 AC Q8VDC2;
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Tmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kiss H., Darai E., Kiss C., Kost-Alimova M., Klein G., Dumaneki J.P.,
 Ruten S.;
 RT "Comparative human/murine sequence analysis of the common eliminated
 RT region 1 from human 3p21.3."
 RL Mamm. Genome 13:646-655(2002).
 DR EMBL: AJ428064; CAD20986.1; -.
 DR MGD: MGI:2446841; Tmem7.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0BE69F2A4D CRC64;
 Query Match 14.5%; Score 96.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 0.96;
 Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;
 QY 5 TVTLGNIGDGRQTLV-----LNPGRVNPNG--VASLSQAGVPALEKRYK 46
 DB 195 TATCSNISSQPSQSKVQMPQASKNQASNPFTKNDPKVCTSKRPAPLSPTSLKAREP 254
 QY 47 RYTVSVQPSNRKRYKQV-----KIQNPT-----ACTANGSCDPSVTRO----- 87
 DB 255 KYTVCSNISSQPSQSKVQMPQASKNQASNPFTKNDPKVCTSKRSTPTPRLLTIQQLSVV 314
 QY 88 -----KYADVTFSPQYSTDEERAFVTELAALASPLLI 122
 DB 315 SPAPAPTCVIQMPSPPTIDGSRADVAKENTRSKTPK-----ALLSPVLY 361
 RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE STANDARD; PRT; 530 AA.
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligeriolysin precursor (Thiol-activated cytolysin).
 GN Name=Isc; seeligeri.
 OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

```

OX NCBI_TaxID=1640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLC;
RX MEDLINE=92182018; PubMed=1543752;
RA Haas A., Dumbsky M., Kreft J.;
RT "Thiololysin genes: complete sequence of ilo from Listeria ivanovi
RL Biochim. Biophys. Acta 1130:81-84(1992).
-1- FUNCTION: Sulfhydryl-activated toxin. Is able to lyse cholesterol
containing membranes. Can be reversibly inactivated by oxidation.
Cholesterol is the receptor for the binding of these toxins to
eukaryotic cell membranes.
-1- SIMILARITY: Belongs to the thiol-activated cytolysin family.
-----
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-----
DR EMBL, X60462; CAA42996.1; -.
DR PIR, S22340; G22340.
DR HSSP, P19995; 1PFO.
DR InterPro, IPR001869; Thiol cytolysin.
DR Pfam, PF01289; Thiol cytolysin; 1.
DR PRINTS, PRO1400; TRCTOLYSIN.
DR ProDom, PD007062; Thiol cytolysin; 1.
DR PROSITE, PS00481; THIOLE CYTOLYSINS; 1.
KW Cytolysis; Hemolysis; Lipid-binding; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 530 Seeligerolysin.
FT SITE 485 485 Binding to cholesterol (By similarity).
SQ SEQUENCE 530 AA; 59181 MW; 416F7A4DD2029866 CRC64;

```

Query Match 13.5%; Score 89.5; DB 1; Length 530;
 Best Local Similarity 25.0%; Pred. No. 5.2;
 Matches 34; Conservative 22; Mismatches 37; Indels 43; Gaps 7;

```

QY 13 KQGRQTLVL--NPRGVNPT-----NGVSLSQAG-----VPALEKRV 48
DB 94 KQSEYIVVEKKKKKGINNADISVINAISSLTYPGALVYANRELVENQPNVLPIVKRDSL 153
QY 49 TVSVSQPSRRKRYKQVKTQNPACTANGSCDPSVTR--QKY-----ADVTFSFTQ 98
DB 154 TLSVDLPGMTKDKNKIFVK--NPTKSNVNNAVNTLVERWMDKYSKAVPINAKIDYS--- 208
QY 99 YSTDERAFVTEIAA 114
DB 209 ----DEMAYSESQLIA 220

```

Search completed: January 4, 2005, 09:16:17
 Job time : 37.2676 secs

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OM protein - protein search, using SW model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-8
Perfect score: 664
Sequence: 1 ALEFVTLGNIGRDKQTLV.....AALLASPLILDAIDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: A_Geneseq_23Sep04:*
 - 2: geneseqp1980s:*
 - 3: geneseqp1990s:*
 - 4: geneseqp2000s:*
 - 5: geneseqp2001s:*
 - 6: geneseqp2002s:*
 - 7: geneseqp2003as:*
 - 8: geneseqp2003bs:*
 - 9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	664	100.0	132	5	ABG94318	Abg94318 POB250 pr
2	664	100.0	132	5	ABG80630	Abg80630 Bacteriop
3	664	100.0	132	6	ABR56454	AbR56454 Bacteriop
4	664	100.0	132	6	ABU09691	Abu09691 Bacteriop
5	664	100.0	132	6	ABR44557	AbR44557 Bacteriop
6	664	100.0	132	7	ADD24132	Add24132 Bacteriop
7	664	100.0	132	7	ADJ82058	Adj82058 Protein f
8	664	100.0	132	7	ADK17146	Adk17146 Virus-11k
9	664	100.0	132	8	ADJ36315	Adj36315 Bacteriop
10	664	100.0	132	8	ADU57161	AdU57161 Phage Qbe
11	664	100.0	132	8	ADK52195	AdK52195 Bacteriop
12	661	99.5	132	5	ABG94316	Abg94316 POB240 pr
13	661	99.5	132	5	ABG80628	Abg80628 Bacteriop
14	661	99.5	132	6	ABR56452	AbR56452 Bacteriop
15	661	99.5	132	6	ABU09689	Abu09689 Bacteriop
16	661	99.5	132	6	ABR44555	AbR44555 Bacteriop
17	661	99.5	132	7	ADD24130	Add24130 Bacteriop
18	661	99.5	132	7	ADJ82056	Adj82056 Protein f
19	661	99.5	132	7	ADK17144	Adk17144 Virus-11k
20	661	99.5	132	8	ADJ36313	Adj36313 Bacteriop
21	661	99.5	132	8	ADU57159	AdU57159 Phage Qbe
22	661	99.5	132	8	ADK52193	AdK52193 Bacteriop
23	658	99.1	132	5	ABG94319	Abg94319 POB250 pr
24	658	99.1	132	5	ABG80631	Abg80631 Bacteriop
25	658	99.1	132	6	ABR56456	AbR56456 Bacteriop

26	658	99.1	132	6	ABU09692	Abu09692 Bacteriop
27	658	99.1	132	6	ABR44559	AbR44559 Bacteriop
28	658	99.1	132	7	ADD24134	Add24134 Bacteriop
29	658	99.1	132	7	ADJ82060	Adj82060 Protein f
30	658	99.1	132	7	ADK17148	Adk17148 Virus-11k
31	658	99.1	132	8	ADJ36317	Adj36317 Bacteriop
32	658	99.1	132	8	ADU57163	AdU57163 Phage Qbe
33	655	98.6	132	5	ABG94320	Abg94320 POB251 pr
34	655	98.6	132	5	ABG80632	Abg80632 Bacteriop
35	655	98.6	132	6	ABR56455	AbR56455 Bacteriop
36	655	98.6	132	6	ABU09693	Abu09693 Bacteriop
37	655	98.6	132	6	ABR44558	AbR44558 Bacteriop
38	655	98.6	132	7	ADD24133	Add24133 Bacteriop
39	655	98.6	132	7	ADJ82059	Adj82059 Protein f
40	655	98.6	132	7	ADK17147	Adk17147 Virus-11k
41	655	98.6	132	7	ADJ36316	Adj36316 Bacteriop
42	655	98.6	132	8	ADU57162	AdU57162 Phage Qbe
43	655	98.6	132	8	ADK52196	AdK52196 Bacteriop
44	655	98.6	132	8	ADK52196	AdK52196 Bacteriop
45	652	98.2	132	5	ABG94233	Abg94233 Bacteriop

ALIGNMENTS

RESULT 1
ID ABG94318 standard; protein; 132 AA.
XX
AC ABG94318;
XX
DT 29-AUG-2003 (revised)
DT 10-DEC-2002 (first entry)
XX
DE POB250 protein.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytoskeletal; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
OS unidentified bacteriophage.
XX
PN MO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002MO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326989P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
DR WPI; 2002-627351/67.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
PS Claim 18; Page 145; 441pp; English.
XX
XX This invention relates to a novel ordered and repetitive antigen array
XX used in the production of vaccines for infectious diseases. The invention
XX also discloses a composition comprising a non-natural molecular scaffold
XX comprising a core particle selected from a core particle of a non-natural
XX origin and a core particle of natural origin and an organism comprising
XX at least one first attachment site, where the organism is connected to
XX the core particle by at least one covalent bond. Also disclosed is an
XX antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abetal-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;

Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGQAGVAPALERKVTVSQPSRNRK 60

DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGQAGVAPALERKVTVSQPSRNRK 60

QY 61 NYKVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALIASPL 120

DB 61 NYKVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALIASPL 120

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

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QY 121 LIDAIDQINPAY 132

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DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVS) NOVARIS PHARMA AG.

PA (MAURER) MAURER P.

PA (LECH) LECHNER F.

PA (ORTM) ORTMANN R.

PA (LUBO) LUBOEND R.

PA (STAUF) STAUFENBIEL M.

PA (FREY) FREY P.

PI Maurer P., Lechner F., Ortmann R., Luegend R., Staufenbiel M., Frey P.,

PI Renner WA, Bachmann M., Tisot A., Sebbel P., Plosssek C,

XX WPI, 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for infectious

XX diseases.

XX Example 18, Page 145; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural

XX molecular scaffold comprising: (i) a core particle selected from: (1) a

XX core particle of a non-natural origin; and (2) a core particle of natural

XX origin; and (ii) an organiser comprising at least one first attachment

XX site, where the organiser is connected to the core particle by at least

XX one covalent bond; (b) an antigen or antigenic determinant with at least

XX one second attachment site, where the antigen or antigenic determinant is

XX amyloid beta peptide (Abeta 1-42) or its fragment, and where the second

XX attachment site is selected from: (i) an attachment site not naturally

XX occurring with the antigen or antigenic determinant; and (ii) an

XX attachment site naturally occurring with the antigen or antigenic

XX determinant, where the second attachment site is capable of association

XX through at least one non-peptide bond to the first attachment site; and

XX where the antigen or antigenic determinant and the scaffold interact

XX through the association to form an ordered and repetitive antigen array.

XX Also included is a process for producing a non-naturally occurring

XX ordered and repetitive antigen array. The composition is used in

XX immunisation and as a vaccine for diseases such as influenza, graft

XX versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult

XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,

XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,

XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia

XX Gravis, immunoproliferative disease lymphadenopathy, immunoblastic

XX angioimmunoproliferative lymphadenopathy, Alzheimer's disease,

XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,

XX osteoporosis and infectious diseases. The antigens are modified to possess

XX a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-

CC virus like particle or bacterial protein (the scaffold protein). The

CC present sequence is bacterial protein or peptide which is coupled to the

CC modified antigen to form the molecular antigen array

CC Sequence 132 AA;

QY Query Match 100.0%; Score 664; DB 5; Length 132;

Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGQAGVAPALERKVTVSQPSRNRK 60

DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPNGVSLGQAGVAPALERKVTVSQPSRNRK 60

QY 61 NYKVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALIASPL 120

DB 61 NYKVQVKIONPTACTANGSCDPSVTROKADYVTFSTQYSTDBERAFVTELAALIASPL 120

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVS) NOVARIS PHARMA AG.

PA (MAURER) MAURER P.

PA (LECH) LECHNER F.

PA (ORTM) ORTMANN R.

PA (LUBO) LUBOEND R.

PA (STAUF) STAUFENBIEL M.

PA (FREY) FREY P.

PI Maurer P., Lechner F., Ortmann R., Luegend R., Staufenbiel M., Frey P.,

PI Renner WA, Bachmann M., Tisot A., Sebbel P., Plosssek C,

XX WPI, 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for infectious

XX diseases.

XX Example 18, Page 145; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural

XX molecular scaffold comprising: (i) a core particle selected from: (1) a

XX core particle of a non-natural origin; and (2) a core particle of natural

XX origin; and (ii) an organiser comprising at least one first attachment

XX site, where the organiser is connected to the core particle by at least

XX one covalent bond; (b) an antigen or antigenic determinant with at least

XX one second attachment site, where the antigen or antigenic determinant is

XX amyloid beta peptide (Abeta 1-42) or its fragment, and where the second

XX attachment site is selected from: (i) an attachment site not naturally

XX occurring with the antigen or antigenic determinant; and (ii) an

XX attachment site naturally occurring with the antigen or antigenic

XX determinant, where the second attachment site is capable of association

XX through at least one non-peptide bond to the first attachment site; and

XX where the antigen or antigenic determinant and the scaffold interact

XX through the association to form an ordered and repetitive antigen array.

XX Also included is a process for producing a non-naturally occurring

XX ordered and repetitive antigen array. The composition is used in

XX immunisation and as a vaccine for diseases such as influenza, graft

XX versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult

XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,

XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,

XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia

XX Gravis, immunoproliferative disease lymphadenopathy, immunoblastic

XX angioimmunoproliferative lymphadenopathy, Alzheimer's disease,

XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,

XX osteoporosis and infectious diseases. The antigens are modified to possess

XX a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-

XX ABR56454;
 AC 28-JUL-2003 (first entry)
 XX
 DT Bacteriophage Q-beta coat protein mutant SEQ ID NO:25.
 XX
 DE Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytotoxic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
 KW antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX Bacteriophage Qbeta.
 OS Synthetic.
 XX WO2003024480-A2.
 XX
 XX 27-MAR-2003.
 PD
 XX 16-SEP-2002; 2002WO-IB004252.
 PF
 XX 14-SEP-2001; 2001US-0318967P.
 PR
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX Bachmann MF, Storni T, Lechner F;
 PI WPI; 2003-363095/34.
 DR
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX
 PS Disclosure; Page 181; 243pp; English.
 XX
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen. Or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antineumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumors and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC65838 to ACC65982 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 132 AA;
 SQ
 Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLETVTLNIGRGQTLVLPNGVPTNGVASTLSQAGAVPALERKVTVSQPSRRNK 60

DB 1 ARLETVTLNIGRGQTLVLPNGVPTNGVASTLSQAGAVPALERKVTVSQPSRRNK 60
 QY 61 NKVQVKIONPRACTANGSCDPSVTRQKADYVTFSTQYSTDEERAFVTELAALASPL 120
 DB 61 NKVQVKIONPRACTANGSCDPSVTRQKADYVTFSTQYSTDEERAFVTELAALASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 RESULT 4
 ABU09691
 ID ABU09691 standard; protein; 132 AA.
 XX
 AC ABU09691;
 XX
 XX 03-JUL-2003 (first entry)
 DT
 XX
 XX Bacteriophage Qbeta mutant coat protein #3.
 DE
 KW Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.
 XX Bacteriophage Qbeta.
 OS WO2003031466-A2.
 XX
 XX 17-APR-2003.
 PD
 XX 07-OCT-2002; 2002WO-BE011219.
 PF
 XX 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX Bachmann M;
 PI WPI; 2003-430264/40.
 DR
 XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 XX
 XX Claim 20; Page 94; 97pp; English.
 PS
 XX The invention describes an angiotensin peptide moiety carrier conjugate
 CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal
 CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC including producing antibodies. This is the amino acid sequence of a
 CC mutant bacteriophage Qbeta coat protein used in the preparation of the
 CC vaccine conjugates of the invention
 XX
 XX Sequence 132 AA;
 SQ
 Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGDGGQTLVLPNGVNPPTNGVASLSQAAGVPALEKRVTVSVSQPSRNK 60
 DB 1 ARLEVTTLGNIGDGGQTLVLPNGVNPPTNGVASLSQAAGVPALEKRVTVSVSQPSRNK 60

QY 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120
 DB 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120

QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132

RESULT 5
 ABR44557
 ID ABR44557 standard; protein; 132 AA.

XX ABR44557;
 AC
 XX
 DT 25-JUL-2003 (first entry)

XX Bacteriophage Q-beta coat protein mutant SEQ ID NO:25.
 XX
 XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KM hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KM immunostimulant; cytotoxic; antiallergic; virucide; antibacterial;
 KM immune response; immunisation; allergy; tumour; breast cancer;
 KM neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KM chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX Bacteriophage Qbeta.
 OS Synthetic.
 OS
 XX
 PN WO2003024481-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 16-SEP-2002; 2002WO-IB004132.
 XX
 PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR/) MAURER P.
 PA (TISSE/) TISSOT A.
 PA (SCHW/) SCHWARZ K.
 PA (WEID/) WEIJERINK E.
 PA (LIP/) LIPOWSKY G.
 PA (PUM/) PUMPENS P.
 PA (CIEL/) CIELENS I.
 PA (RENN/) RENNOFA R.
 XX
 PI Maurer P, Tisseot A, Schwarz K, Weijerink E, Lipowsky G,
 PI Pumpens P, Cieleus I, Rennofa R, Bachmann MF, Storm T;
 XX
 DR WPI; 2003-354564/33.
 XX
 PT New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX
 PS Disclosure; Page 260-261; 322pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC creating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the vaccine;
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or creating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention

XX Sequence 132 AA;
 SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGDGGQTLVLPNGVNPPTNGVASLSQAAGVPALEKRVTVSVSQPSRNK 60
 DB 1 ARLEVTTLGNIGDGGQTLVLPNGVNPPTNGVASLSQAAGVPALEKRVTVSVSQPSRNK 60

QY 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120
 DB 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120

QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132

RESULT 6
 ADD24132
 ID ADD24132 standard; protein; 132 AA.
 XX
 AC ADD24132;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX Bacteriophage Qbeta coat protein mutant Qbeta-250.
 DE
 XX vaccine composition; virus-like particle; core particle;
 KM first attachment site; antigen; antigenic determinant; prion protein;
 KM PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KM prion disease; Bovine Spongiform Encephalopathy; BSE;
 KM Creutzfeldt-Jakob Disease; coat protein; mutant; muten.
 XX
 OS Synthetic.
 OS Bacteriophage Qbeta.
 OS
 XX
 PN WO2003059386-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-EB000460.
 XX
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PI Bachmann M, Maurer P, Fellicioli E, Renner WA;
 XX
 DR WPI; 2003-598483/56.
 XX
 PT A vaccine composition for preventing or treating prion diseases (e.g.

PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PR phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.

PS Example 1, SEQ ID NO 25, 246bp, English.

XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (Prp)
 CC or its dimer, or a Prp peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. Creutzfeldt-Jakob
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC disease. The present sequence is the amino acid sequence of a mutant coat
 CC protein from Bacteriophage Qbeta which may be used during the creation of
 CC the vaccine composition of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NRVQVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 61 NRVQVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTELAALLASPL 120
 QY 121 LIDAIIDQINPAY 132
 DB 121 LIDAIIDQINPAY 132

RESULT 7

ADJ82058
 ID ADJ82058 standard; protein; 132 AA.

XX ADJ82058;
 AC
 XX
 DT 06-MAY-2004 (first entry)
 DE Protein for RANKL antigen array to treat bone disease.
 XX
 KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
 KW bone disease; encephalopathy; immune system stimulation.
 XX
 OS Unidentified.
 XX
 PN WO2003039225-A2.
 PD
 XX
 PF 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-EP012449.
 XX
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-18000166.
 PR 19-JUL-2002; 2002US-0396635P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PI Bachmann M, Maurer P, Spohn G;
 XX
 DR WPI; 2003-441430/41.
 XX

PT New compositions comprising a core particle and at least one antigen or
 PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
 PT of bone diseases, particularly mammalian encephalopathies.

XX Disclosure; SEQ ID NO 25, 222bp; English.

XX The invention relates to a composition comprising a core particle having
 CC at least one first attachment site, and at least one antigen or antigenic
 CC determinant having at least one second attachment site. The antigen or
 CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
 CC peptide. The second attachment site is (non-) naturally occurring with
 CC the antigen or antigenic determinant, and is capable of association to
 CC the first attachment site. The antigen or antigenic determinant and the
 CC core particle interact through the association to form an ordered and
 CC repetitive antigen array. The composition is useful as a medicament, or
 CC for the manufacture of a medicament for treating bone diseases. The
 CC composition is especially useful for as a vaccine for therapy or
 CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
 CC and for stimulating mammalian immune system. This sequence represents a
 CC protein of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NRVQVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 61 NRVQVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDERAFVTELAALLASPL 120
 QY 121 LIDAIIDQINPAY 132
 DB 121 LIDAIIDQINPAY 132

RESULT 8

ADK17146
 ID ADK17146 standard; peptide; 132 AA.

XX ADK17146;
 AC
 XX
 DT 06-MAY-2004 (first entry)
 DE Virus-like particle repetitive antigen array peptide #25.
 XX
 KW antiallergic; antiasthmatic; cyostatic; vaccine; virus-like particle;
 KW interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;
 KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
 XX
 OS Unidentified.
 XX
 PN WO2003040164-A2.
 PD
 XX
 PF 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-EP012455.
 XX
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-18000166.
 PR 19-JUL-2002; 2002US-0396635P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PI Bachmann M, Jennings G, Sonderegger I;
 XX
 DR WPI; 2003-441518/41.
 XX

PT Composition comprising an ordered and repetitive antigen or antigenic
 PT determinant array, useful as a medicament, or for manufacturing a
 PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's lymphoma.
XX
PS Disclosure; SEQ ID NO 25; 245bp; English.
XX
CC The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC compositions are useful as medicaments, or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Gaps 0;
Matches 132; Conservative 0; Indels 0;
QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
Db 121 LIDAIIDQINPAY 132

RESULT 9
ADJ36315
ID ADJ36315 standard; protein; 132 AA.
AC ADJ36315;
XX
DT 22-APR-2004 (first entry)
XX
DE Bacteriophage Qbeta coat protein virus-like particle mutant M10K.
XX
KW anti-allergic; cytostatic; virucide; immunostimulant; vaccine;
KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
KW chronic disease; chronic viral disease; bacteriophage Qbeta;
KW coat protein; VLP; adjuvant; mutant; mutein.
XX
OS Bacteriophage Qbeta.
XX
PN WO2004000351-A1.
XX
PD 31-DEC-2003.
XX
PF 20-JUN-2003; 2003WO-EP006541.
XX
PR 20-JUN-2002; 2002US-0389898P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Renner WA;
XX
DR WPI; 2004-108361/11.
XX
PT New compositions comprising a virus-like particle (VLP), an
PT immunostimulatory substance bound to the VLP, and an antigen mixed with
PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
XX
PS Disclosure; SEQ ID NO 16; 252bp; English.
XX
CC The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC disease such as allergic, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
CC coat protein mutant, a virus like particle (VLP) that can be used in the
CC adjuvant of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Gaps 0;
Matches 132; Conservative 0; Indels 0;
QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBRAVFTTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
Db 121 LIDAIIDQINPAY 132

RESULT 10
ADJ67161
ID ADJ67161 standard; protein; 132 AA.
AC ADJ67161;
XX
DT 06-MAY-2004 (first entry)
XX
DE Phage Qbeta coat protein mutant Qbeta 250 for antigen display array.
XX
KW anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
KW antigenic array.
XX
OS Bacteriophage Qbeta.
XX
PN WO2004009124-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-EP007849.
XX
PR 19-JUL-2002; 2002US-0396638P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Fulurija A;
XX
DR WPI; 2004-132866/13.
XX
PT New composition comprising a core particle having a first attachment site
PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
PT peptide having a second attachment site, useful for treating obesity.
XX
PS Disclosure; SEQ ID NO 19; 175bp; English.
XX
CC The invention relates to a new composition comprising: (i) a core
CC particle with at least one first attachment site; and (ii) at least one
CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is shrelin or a shrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the shrelin or a
 CC shrelin peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a Bacteriophage
 CC Qbeta coat protein mutant which can be used as part of the repetitive or
 CC antigenic array.

SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETLAALLASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETLAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132

RESULT 11

ADK52195 standard; protein; 132 AA.

AC ADK52195;

DT 20-MAY-2004 (first entry)

DE Bacteriophage Qbeta coat protein mutant K2R K13R.

XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;

KM core particle; antigen array; Alzheimer's disease; RNA bacteriophage;

XX coat protein; CP; mutant; mutein.

OS Bacteriophage Qbeta.

XX Synthetic.

OS Bacteriophage Qbeta.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
 PT such as Alzheimer's disease.

XX Example 1; SEQ ID NO 19, 184pp; English.

PS The invention describes a novel composition comprising a virus-like core
 CC particle with at least one attachment site, and an antigenic amyloid beta
 CC 1-6 peptide. The new composition comprises a core particle with at least
 CC one first attachment site; and at least one antigen or antigenic
 CC determinant with at least one second attachment site, where the antigen
 CC or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
 CC second attachment site comprises an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; or an attachment
 CC site naturally occurring with the antigen or antigenic determinant. The
 CC second attachment site is capable of association to the first attachment
 CC site and the beta 1-6 peptide and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC composition is useful for the manufacture of a medicament for treating
 CC Alzheimer's disease and related diseases. This is the amino acid sequence
 CC of an RNA bacteriophage Qbeta coat protein mutant that can be used in the
 CC preparation of the compositions and vaccines of the invention.

SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 8.2e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 DB 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVSLSQAGAVPALERKVTVSQPSRNK 60
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETLAALLASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETLAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132

RESULT 12

ABG94316 standard; protein; 132 AA.

AC ABG94316;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

DE POB240 protein.

XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;

KM cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;

XX vaccine; infectious disease.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX unidentified bacteriophage.

XX WPI; 2002-627351/67.
 DR Bacteriophage Qbeta.
 XX Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Claim 18; Page 144; 441pp; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 132 AA:
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLETTVGNIGRDKQKTLVNPNGVNPVTSLSQAGVAPLKERVTVSVQSPNNRK 60
 DB 1 AKLETVGNIGRDKQKTLVNPNGVNPVTSLSQAGVAPLKERVTVSVQSPNNRK 60
 QY 61 NYKQVQVIONPTACTANGSCDPSTVTRQKADVTFFSYSTDEBRARFTELALIASPL 120
 DB 61 NYKQVQVIONPTACTANGSCDPSTVTRQKADVTFFSYSTDEBRARFTELALIASPL 120
 QY 121 LIDALDQLNPAY 132
 DB 121 LIDALDQLNPAY 132
 RESULT 13
 ABG80628
 ID ABG80628 standard; protein; 132 AA.
 XX
 XX ABG80628;
 DT 29-NOV-2002 (first entry)
 XX
 XX Bacteriophage Q-beta A1 coat protein mutant Qbeta-240.
 DE
 XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; Igs-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;

KM enterokinase; cysteine-containing linker.
 XX
 XX Bacteriophage Qbeta.
 OS Synthetic.
 XX
 XX WO200256907-A2.
 XX
 XX 25-JUL-2002.
 XX
 XX 21-JAN-2002; 2002WO-1B000168.
 XX
 XX 19-JAN-2001; 2001US-0262379P.
 XX 04-MAY-2001; 2001US-0288549P.
 XX 05-OCT-2001; 2001US-0326998P.
 XX 07-NOV-2001; 2001US-0331045P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER P.
 PA (ORTM/) ORTMANN R.
 PA (LUEO/) LUEOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Seibel P, Floseek C;
 DR WPI; 2002-636514/68.
 XX
 XX Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 XX Example 18; Page 144; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (i) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, Igs-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 CC
 XX
 SQ Sequence 132 AA:
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 Db 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 QY 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFFSTQYSTDBERAFVRTTELAALLASPL 120
 Db 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFFSTQYSTDBERAFVRTTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 Db 121 LIDAIDQINPAY 132

RESULT 14
 ABR56452
 ID ABR56452 standard; protein; 132 AA.
 XX ABR56452;
 XX 28-JUL-2003 (first entry)
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:23.
 XX
 XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antihydrolytic; antidiabetic; neuroprotective; nootropic; osteopathic;
 KW antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 XX Bacteriophage Qbeta.
 OS Synthetic.
 OS
 XX WO2003024480-A2.
 XX
 XX 27-MAR-2003.
 PD
 XX 16-SEP-2002; 2002WO-18004252.
 PF
 XX 14-SEP-2001; 2001US-0318967P.
 PR
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX Bachmann MF, Storni T, Lechner F;
 PI
 XX WPI; 2003-363095/34.
 DR
 XX
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 PT
 XX
 XX Disclosure; Page 179-180; 243pp; English.
 PS
 XX
 XX The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antihydrolytic, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antineumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an

CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumors and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SO Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 6; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 Db 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVSQPSRNK 60
 QY 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFFSTQYSTDBERAFVRTTELAALLASPL 120
 Db 61 NKVQVKIOMPACTANGSCDPSVTRQKADVTFFSTQYSTDBERAFVRTTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 Db 121 LIDAIDQINPAY 132

RESULT 15
 ABU09689
 ID ABU09689 standard; protein; 132 AA.
 XX
 XX ABU09689;
 AC
 XX
 XX 03-JUL-2003 (first entry)
 DT
 XX
 XX Bacteriophage Qbeta mutant coat protein #1.
 DE
 XX
 XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.
 KW
 XX
 XX Bacteriophage Qbeta.
 OS
 XX WO2003031466-A2.
 PN
 XX
 XX 17-APR-2003.
 PD
 XX
 XX 07-OCT-2002; 2002WO-EP011219.
 PF
 XX
 XX 05-OCT-2001; 2001US-0326998P.
 PR
 XX 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-18000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX Bachmann M;
 PI
 XX WPI; 2003-430264/40.
 DR
 XX
 XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 PT
 XX
 XX Claim 20; Page 93-94; 97pp; English.
 PS
 XX
 XX The invention describes an angiotensin peptide moiety carrier conjugate

CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal
 CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC including producing antibodies. This is the amino acid sequence of a
 CC mutant bacteriophage Qbeta coat protein used in the preparation of the
 CC vaccine conjugates of the invention
 XX

Sequence 132 AA:

Query Match 99.5%; Score 661; DB 6; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1.9e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	ARLEVTIGNIGRDKQTLVNPGRVNPPTNGVASLSQAGAVPALERKRVTVSVQPSRNRK	60
		:	
Db	1	AKLETVTIGNIGRDKQTLVNPGRVNPPTNGVASLSQAGAVPALERKRVTVSVQPSRNRK	60
		:	
QY	61	NYKVQVKIQNPPTACTANGSCDPSVTROKVDVTFSTQYSTDERAFVRTETLAALIASPL	120
Db	61	NYKVQVKIQNPPTACTANGSCDPSVTROKVDVTFSTQYSTDERAFVRTETLAALIASPL	120
QY	121	LIDAIIDQINPAY	132
Db	121	LIDAIIDQINPAY	132

Search completed: January 4, 2005, 09:11:01
 Job time : 39.6824 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:05:21 ; Search time 10.3622 Seconds
(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-8
Perfect score: 664
Sequence: 1 ALEVTYLTGICNRDQKQTLV.....AALLASPLIDALIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues
Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.5	12.3	626	4 US-09-485-717-2	Sequence 2, Appl1
2	81.5	12.3	626	4 US-09-948-722-2	Sequence 2, Appl1
3	75	11.3	409	4 US-09-328-352-4249	Sequence 4249, Ap
4	71.5	10.8	818	4 US-09-252-991A-16691	Sequence 16691, A
5	71.5	10.8	916	4 US-09-252-991A-23637	Sequence 23637, A
6	70.5	10.6	502	4 US-09-270-767-44620	Sequence 44620, A
7	69.5	10.5	129	1 US-08-090-148-1	Sequence 1, Appl1
8	69	10.4	300	4 US-09-302-626B-182	Sequence 182, App
9	69	10.4	622	4 US-09-302-626B-185	Sequence 185, App
10	69	10.4	766	4 US-09-538-092-216	Sequence 216, App
11	69	10.4	1073	4 US-09-206-942-49	Sequence 49, Appl
12	69	10.4	1079	4 US-09-206-942-47	Sequence 47, Appl
13	68.5	10.3	381	4 US-09-198-452A-745	Sequence 745, App
14	68.5	10.3	383	3 US-09-045-186-2	Sequence 2, Appl1
15	68.5	10.3	384	3 US-08-232-144-4	Sequence 4, Appl1
16	68.5	10.3	384	2 US-08-555-268A-15	Sequence 15, Appl
17	68.5	10.3	384	2 US-09-200-673-15	Sequence 15, Appl
18	68.5	10.3	384	4 US-10-013-846-4	Sequence 4, Appl1
19	68.5	10.3	384	4 US-09-708-392-9	Sequence 9, Appl1
20	68.5	10.3	384	5 PCT-US93-05039-3	Sequence 3, Appl1
21	68.5	10.3	411	5 US-08-817-869-3	Sequence 3, Appl1
22	68.5	10.3	411	5 PCT-US95-14377-3	Sequence 3, Appl1
23	68.5	10.3	733	4 US-09-248-796A-16565	Sequence 16565, A
24	68	10.2	316	4 US-09-270-767-43925	Sequence 43925, A
25	68	10.2	316	4 US-09-270-767-59311	Sequence 59311, A
26	68	10.2	415	4 US-09-252-991A-29602	Sequence 29602, A
27	67.5	10.2	424	3 US-09-173-581-7	Sequence 7, Appl1

28	67.5	10.2	424	3 US-09-420-915-7	Sequence 7, Appl1
29	67.5	10.2	428	3 US-09-134-001C-2885	Sequence 2885, Ap
30	67.5	10.2	1328	3 US-08-781-891-76	Sequence 76, Appl
31	67.5	10.2	1328	4 US-09-618-166-76	Sequence 76, Appl
32	67	10.1	322	4 US-09-328-352-6759	Sequence 6759, Ap
33	67	10.1	632	4 US-09-976-594-41	Sequence 41, Appl
34	66.5	10.0	279	3 US-08-397-411-13	Sequence 13, Appl
35	66.5	10.0	398	6 5495001-9	Patent No. 5495001
36	66.5	10.0	915	4 US-09-206-942-35	Sequence 35, Appl
37	66.5	10.0	1220	4 US-09-206-942-28	Sequence 28, Appl
38	66.5	10.0	1222	4 US-09-206-942-37	Sequence 37, Appl
39	66.5	10.0	1226	4 US-09-206-942-26	Sequence 26, Appl
40	66.5	10.0	1228	4 US-09-206-942-34	Sequence 34, Appl
41	66	9.9	187	3 US-08-916-246-12	Sequence 12, Appl
42	66	9.9	187	4 US-09-949-186-12	Sequence 12, Appl
43	66	9.9	1036	2 US-08-720-484A-5	Sequence 5, Appl1
44	66	9.9	1036	3 US-08-953-822A-5	Sequence 5, Appl1
45	66	9.9	1036	4 US-09-398-239-5	Sequence 5, Appl1

ALIGNMENTS

```
RESULT 1
US-09-485-717-2
; Sequence 2, Application US/09485717
; Patent No. 6673353
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan
; APPLICANT: Hees, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 16862PUS
; CURRENT APPLICATION NUMBER: US/09/485,717
; PRIOR APPLICATION NUMBER: EP 97114614.7
; PRIOR FILING DATE: 1997-08-22
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/EP98-05109
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2

Query Match          12.3%; Score 81.5; DB 4; Length 626;
Best Local Similarity 22.0%; Pred. No. 0.3;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQLVL-----NPRGVNPNVGVASLSQAG-----VPALEKRV 48
      |||:|:|
DB 138 KGNENYIVAEKKKKSINQNNADIQVNAISLTPALVKANSELVENOPDVLVPRDSL 197
QY 49 TVSVSQPSNRKKYKQVQIOWPCTANGSCDPSVTR-----OKYADVFSTGYSTD 102
      |||:|:|
DB 198 TLSIDIPGNTNQNKNVVK--NATKSNVNNVAVTLVERNNKTAQVAPNVS---AKIDVD 252
QY 103 EERAFVETELAA 114
      |||:|:|
DB 253 DEMAYGESQLIA 264

RESULT 2
US-09-948-722-2
; Sequence 2, Application US/09948722
; Patent No. 6776993
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan H. E.
; APPLICANT: Hees, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine
```

```
FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
OTHER INFORMATION: escape domain
US-09-948-722-2
```

Query Match 12.3%; Score 81.5; DB 4; Length 626;

Best Local Similarity 22.0%; Pred. No. 0.3;

Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

```
QY 13 RDGKQTLVLT-----NPRGVNPTNGVASLSQAGA-----VPALKRV 48
DB 138 KDGEYIVVEKKKSNQNNADIQVNAISLTYPGALVKNSELVENQPDVLVKKRDSL 197
QY 49 TVVSQPSRNRKQVQKIQNPACFANGSCDPSVTR-----QKADTFSTQSTD 102
DB 198 TLISIDLGMTNQDKIVK--NATKSNVNNAVNLVLRMNEKKAQAPVNS---AKIDYD 252
QY 103 EERAFVRETEAA 114
DB 253 DEMAYSESOLIA 264
```

RESULT 3

US-09-328-352-4249

Sequence 4249, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4249

LENGTH: 409

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-4249

Query Match 11.3%; Score 75; DB 4; Length 409;

Best Local Similarity 25.2%; Pred. No. 1;

Matches 31; Conservative 19; Mismatches 51; Indels 22; Gaps 5;

```
QY 13 RDGKQTLVLTNPR-----GVNPTNGVASLSQAGAVPALERKRVTV--SVSQPSRNRKRYKVQ 65
DB 118 RGTGRLNANVVRNALISPAVNPVDGTPP-----IAKPRQRLTIRLLAPFGTGSN--A 169
QY 66 VKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVRETEAAALLASPLLDIAI 125
DB 170 IAVLRETFGTNNAALVENTAKRYSEITF-----EEVMSVKTIATLHMLKASKKQILDDL 222
QY 126 DDL 128
DB 223 PQL 225
```

```
RESULT 4
US-09-252-991A-16691
Sequence 16691, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16691
LENGTH: 818
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16691
```

Query Match 10.8%; Score 71.5; DB 4; Length 818;

Best Local Similarity 31.4%; Pred. No. 8.7;

Matches 27; Conservative 9; Mismatches 27; Indels 23; Gaps 4;

```
QY 1 ARLEVTTLGNIGRDGKQTLVLTNPRGVNPTNG-----VASL-----SQAGVPALEK 46
DB 607 ARLRGV--LQGLRDGSAALRTTGEVNRGAIWALGLVAAALLPRTQGEVAAABG 665
QY 47 RV-----TVVSQPSRNRKRYKV 64
DB 666 RIALDDPAAALGDSHGERVRRYGV 691
```

RESULT 5

US-09-252-991A-23637

Sequence 23637, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23637

LENGTH: 916

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23637

Query Match 10.8%; Score 71.5; DB 4; Length 916;

Best Local Similarity 22.9%; Pred. No. 10;

Matches 27; Conservative 17; Mismatches 53; Indels 21; Gaps 4;

```
QY 9 GNIGRDG-----KQTLVLTNPRGVNPTNGVASLSQAGAVPALERKRVTVS-----QP 55
DB 789 GILGEGGLARLRAIVQARRIDPFQGLAALPVGGLPALQMEDPAFGSLDQRWQA 848
QY 56 SRNRKRYVQVQKIQNPAC--TANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVRT 110
DB 849 EERAFVRETEAAERHPCSTIEANADCPUSADAGK-----PWTIPSDSATRWALKT 901
```

RESULT 6

US-09-270-767-44620

Sequence 44620, Application US/09270767

```

; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 44620
; LENGTH: 502
; TYPE: PR
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44620

Query Match      10.6%; Score 70.5; DB 4; Length 502;
Best Local Similarity 24.2%; Pred. No. 5.4;
Matches 29; Conservative 20; Mismatches 52; Indels 19; Gaps 4;

Qy 18 TLVLRGVNPTNGVASLSQAGVPALEKRYTVSVSQP-----SRNRKRYVQYKIQN 70
Db 258 TIAVN--ISPSPPPPQPIVEPEQVENSVTVTVASPEVPVAXARNDXRTSTIKX 314
Qy 71 PRACTANGSCDPVTRQKADVTFFSFQ-----YSTDERAFVPT--ELALLASPL 121
Db 315 AXVAVKFFCTSSATHTSTRCISSYVSQSLGSPPLGXADKDFVTLXLAFFISSPL 374

RESULT 7
US-08-090-148-1
; Sequence 1, Application US/08090148
; Patent No. 5534257
; GENERAL INFORMATION:
; APPLICANT: Mastico, Robert Allan
; APPLICANT: Stockley, Peter George
; APPLICANT: Talbot, Simon John
; TITLE OF INVENTION: Antigen-Presenting Capsid with
; TITLE OF INVENTION: Fusion MS2-Coat Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roseman & Collin
; STREET: 575 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10022-2585
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5", 1.44MB
; COMPUTER: IBM PS2-486
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,148
; FILING DATE: 08/11/93
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 9101550.3
; FILING DATE: 01/24/91
; APPLICATION NUMBER: PCT/GB92/00124
; FILING DATE: 01/22/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Nissenbaum, Israel
; REGISTRATION NUMBER: 27,582
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 940-8636
; TELEFAX: (212) 940-6404
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 AMINO ACIDS
; TYPE: AMINO ACID

```

```

; TOPOLOGY: NOT RELEVANT
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: VIRUS
; FEATURE:
; NAME/KEY: Coat protein from MS2-RNA
; NAME/KEY: Bacteriophage
; LOCATION: Location 1 through 129 below
; LOCATION: represents entire MS2 coat
; LOCATION: protein in the published
; LOCATION: sequence.
; PUBLICATION INFORMATION:
; AUTHORS: Min Jou, W.; Haegeman, G.;
; AUTHORS: Ysebaert, M.; Piers, W.
; TITLE: Nucleotide sequence of the
; TITLE: gene coding for the
; TITLE: Bacteriophage MS2 coat protein
; JOURNAL: Nature
; VOLUME: 237
; PAGES: 82-88
; DATE: 1972
US-08-090-148-1

Query Match      10.5%; Score 69.5; DB 1; Length 129;
Best Local Similarity 25.0%; Pred. No. 0.83;
Matches 24; Conservative 16; Mismatches 43; Indels 13; Gaps 2;

Qy 27 NPNQVIA-----SLSQAGVPALEKRYTVSVSQPBRNRKRYVQYKIQNPRACTANGSC 80
Db 24 NPNQVIAEWISSNSRQA-----YKVCISVQSSAQNRKRYTVKVEKVAQTQTGVGE 76
Qy 81 DSVTRQKADVTFFSFQYSTDERAFVPTLALL 116
Db 77 LPVAAMRSTLNMELTIPRATNSDCELIVKAGGL 112

RESULT 8
US-09-302-626B-182
; Sequence 182, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Masiqani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizzi, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIORITY APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 182
; LENGTH: 300
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pspsa
US-09-302-626B-182

Query Match      10.4%; Score 69; DB 4; Length 300;
Best Local Similarity 23.2%; Pred. No. 3.7;
Matches 38; Conservative 17; Mismatches 51; Indels 58; Gaps 7;

Qy 10 NIGRDKQTLVINGVNPNGVASSLSQAGV-----PALEKRYT 49
Db 5 NVHRDQKSMQDEASAVRT--GAASVSARAAFGPRMAFVWMLGVAAFPAPASGII 63
Qy 50 VSVSQPSNR-----KNRYVQYKIQNPACTANGSCDPVTRQKADVTFFSFQYSTDE 103
Db 64 ADKSAFKNOQAVILQFANGLPQVNIQTPS-----SQGVSVNR-----FKQFDVDE 108

```

QY 104 E-----RAFRTELAAAL-----ASPLIDAIIDOLNPA 131
DB 109 KGVILNNSRNTOTQLOGWIOGNPHILARGEARVIVNOIDSSNPS 152

RESULT 9

US-09-302-626B-185
Sequence 185, Application US/09302626B
Patent No. 6709660
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Masiarant, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 185
LENGTH: 622
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: pspa
US-09-302-626B-185

Query Match 10.4%; Score 69; DB 4; Length 622;
Best Local Similarity 23.2%; Pred. No. 12;
Matches 38; Conservative 17; Mismatches 51; Indels 58; Gaps 7;

QY 10 NIGRDKQTLVNLPRGVNPTNGVASLSQAGAV-----PALEKRVTV 49
DB 23 NVHRDGSQMDSEASAVRVT-GAASVSSABAFGRMAAFSVMALGVAAFSAPASGII 81
QY 50 VVSQSPERAN-----KNYKVOYKIQNPACTANGSCDPSVTQKADVTFFSTQYSTDE 103
DB 82 ADKSAPKNOQAVIILQTNAGLIPQVNIQTPS-----SGGVSVNR-----FKQFVVD 126
QY 104 E-----RAFRTELAAAL-----ASPLIDAIIDOLNPA 131
DB 127 KGVILNNSRNTOTQLOGWIOGNPHILARGEARVIVNOIDSSNPS 170

RESULT 10

US-09-538-092-216
Sequence 216, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Tracy A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurataseqFormatter Version 0.9
SEQ ID NO 216
LENGTH: 766
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURES:
NAME/KEY: misc_feature
LOCATION: (0)...(0)

OTHER INFORMATION: Polypeptide Accession Number YDR490C
US-09-538-092-216

Query Match 10.4%; Score 69; DB 4; Length 766;
Best Local Similarity 23.8%; Pred. No. 16;
Matches 36; Conservative 25; Mismatches 60; Indels 30; Gaps 7;

QY 5 TWTLAGNI---GRDQKOTLVNPRGVNPTNGVASLSQAGAV-----PALEKRVTVSVS 53
DB 431 TVKMANLQLAGNHADTPICQAPATSGEHSVISMRTATAPFKDVTSPCKLSKSTSVR 490
QY 54 QPSRNRKNKYOVKIQNPACTANGSCDPSVT-----RQKADVTFFSTQYSTDEER 105
DB 491 SASNNTDREVIOKQVSKNRASVSS-----PSISTSRGRKNRSDPAFWSRYLQNMND-ER 545
QY 106 AFRTELAA-----LASPLIID--AIDOLNP 130
DB 546 VILMKREVALSTNLNEDSPVLENVLDYKNP 576

RESULT 11

US-09-206-942-49
Sequence 49, Application US/09206942
Patent No. 6432669
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
FILE REFERENCE: 1038-861 MTS:jb
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 1073
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-206-942-49

Query Match 10.4%; Score 69; DB 4; Length 1073;
Best Local Similarity 22.0%; Pred. No. 28;
Matches 27; Conservative 26; Mismatches 52; Indels 18; Gaps 4;

QY 4 EYTTLAGNIGRDGKQTLVNLPRG-----VNPTNGVASLSQAGAVPALERKRVTVSVS 54
DB 766 KTLTVGNV--SGNTVTVTANRGALTTLAGSTINGNGVTTSSQSGEIGBVTGKTVSVTA 823
QY 55 PSNR--RNKYKVOYKIQNPACTANGSCDPSVTQKADVTFFSTQYSTDEERAFVTE 111
DB 824 TAGSLTVKGAKINMREGTATITLASSG-----KLTEASSNIISAKQVQLSNQDGSIAQG 879
QY 112 LAA 114
DB 880 ISA 882

RESULT 12

US-09-206-942-47
Sequence 47, Application US/09206942
Patent No. 6432669
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
FILE REFERENCE: 1038-861 MTS:jb
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08

EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 1079
TYPE: PR1
ORGANISM: Haemophilus influenzae
US-09-206-942-47

Query Match 10.4%; Score 69; DB 4; Length 1079;
Best Local Similarity 22.0%; Pred. No. 28;
Matches 27; Conservative 26; Mismatches 52; Indels 18; Gaps 4;

QY 4 EYTLNIGRDKQTLVLPNRG-----VNPTNGVASTSQAGVPALEKRVTSVSQ 54
DB 772 KILTVGVN--SGVTVTYVTRNGALITLAGSTINGTVTSOSGEIGSVTGKTVSVTA 829
QY 55 PSRN---RKNYKQVQKIONPACTANGSCDPSVTRQKADVTFPSFTQYSTDEERAFVTE 111
DB 830 TAGSLTVKGAQKINATEGATLTVASSG---KLTTEASSNITSAGQVDSLDAQDSIAGQ 885
QY 112 LAA 114
DB 886 ISA 888

RESULT 13
US-09-198-452A-745
Sequence 745, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 745
LENGTH: 381
TYPE: PR1
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: SITE
LOCATION: 1...381
OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-745

Query Match 10.3%; Score 68.5; DB 4; Length 381;
Best Local Similarity 19.8%; Pred. No. 6.2;
Matches 26; Conservative 27; Mismatches 63; Indels 15; Gaps 3;

QY 3 LETVTGNTGRDQKQTLVLPNRGVPNTNGVASTSQAGVPALEKRVTSVSQPSRRNKNY 62
DB 6 VKTVIL-NIGRKILGIGIKKKKIGXSGFLDLV-----LIGVSGQRPRTSANY 56
QY 63 KQVQKIONPACTANGSCDPSVTRQKADVTFPS-----FTQYSTDEERAFVTELAAL 116
DB 57 KHNIRDEKLAACPKNSAASLSAKSKSHTKTTPGSIPIKSVSKEDATQDKTFOKTSGSAPP 116
QY 117 ASPLLDALID 127
DB 117 AKPTLKEEE 127

RESULT 14
US-09-045-186-2
Sequence 2, Application US/09045186
Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Baez, Melynn

APPLICANT: Cates, Carolyn A.
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-045-186-2

Query Match 10.3%; Score 68.5; DB 3; Length 383;
Best Local Similarity 25.0%; Pred. No. 6.3;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVLPNRGVPNTN-----GVA---SLSQAGVPALEKRVTSVSQPSRRNKYKQVK 67
DB 138 RHQILINPRGMRNNHAYGVIVWVLAASSLPFLIYQ--VMTDEPRON----- 186
QY 68 IQNPACTANGSCDPSVTRQKADVTFPSFTQYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYDKYVCFDQPSDSHRLSYTLVLVL 218

RESULT 15
US-08-232-144-4
Sequence 4, Application US/08232144
Patent No. 5571695
GENERAL INFORMATION:
APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: 555 13th St, N.W., Suite 701-East
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,144
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-8
Perfect score: 664
Sequence: 1 ARLETTYLGNIGRDGKQTLV.....AALLASPLTDAIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgnt2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
 - 2: /cgnt2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
 - 3: /cgnt2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
 - 4: /cgnt2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
 - 5: /cgnt2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
 - 6: /cgnt2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgnt2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
 - 8: /cgnt2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
 - 9: /cgnt2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep.*
 - 10: /cgnt2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
 - 11: /cgnt2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
 - 12: /cgnt2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
 - 13: /cgnt2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
 - 14: /cgnt2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
 - 15: /cgnt2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
 - 16: /cgnt2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*
 - 17: /cgnt2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
 - 18: /cgnt2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
 - 19: /cgnt2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
 - 20: /cgnt2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	14	US-10-243-739-25 Sequence 25, App1
2	664	100.0	132	14	US-10-244-065-25 Sequence 25, App1
3	664	100.0	132	14	US-10-289-454-25 Sequence 25, App1
4	664	100.0	132	14	US-10-050-902-257 Sequence 257, App
5	664	100.0	132	14	US-10-050-898-257 Sequence 257, App
6	664	100.0	132	14	US-10-346-190-25 Sequence 25, App1
7	664	100.0	132	15	US-10-465-811-16 Sequence 16, App1
8	664	100.0	132	15	US-10-289-456-25 Sequence 25, App1
9	664	100.0	132	15	US-10-622-064-8 Sequence 8, App1
10	664	100.0	132	15	US-10-622-124-19 Sequence 19, App1
11	664	100.0	132	16	US-10-622-087-19 Sequence 19, App1
12	661	99.5	132	14	US-10-243-739-23 Sequence 23, App1
13	661	99.5	132	14	US-10-244-065-23 Sequence 23, App1

14	661	99.5	132	14	US-10-289-454-23	Sequence 23, App1
15	661	99.5	132	14	US-10-050-902-255	Sequence 255, App
16	661	99.5	132	14	US-10-050-898-255	Sequence 255, App
17	661	99.5	132	14	US-10-346-190-23	Sequence 23, App1
18	661	99.5	132	15	US-10-465-811-14	Sequence 14, App1
19	661	99.5	132	15	US-10-289-456-23	Sequence 23, App1
20	661	99.5	132	15	US-10-622-064-6	Sequence 6, App1
21	661	99.5	132	15	US-10-622-124-17	Sequence 17, App1
22	661	99.5	132	16	US-10-622-087-17	Sequence 17, App1
23	668	99.1	132	14	US-10-243-739-27	Sequence 27, App1
24	668	99.1	132	14	US-10-244-065-27	Sequence 27, App1
25	668	99.1	132	14	US-10-289-454-27	Sequence 27, App1
26	668	99.1	132	14	US-10-050-902-258	Sequence 258, App
27	668	99.1	132	14	US-10-050-898-258	Sequence 258, App
28	668	99.1	132	14	US-10-346-190-27	Sequence 27, App1
29	668	99.1	132	15	US-10-465-811-18	Sequence 18, App1
30	668	99.1	132	15	US-10-289-456-27	Sequence 27, App1
31	668	99.1	132	15	US-10-622-064-10	Sequence 10, App1
32	668	99.1	132	16	US-10-622-124-21	Sequence 21, App1
33	668	99.1	132	15	US-10-622-087-21	Sequence 21, App1
34	655	98.6	132	14	US-10-243-739-26	Sequence 26, App1
35	655	98.6	132	14	US-10-244-065-26	Sequence 26, App1
36	655	98.6	132	14	US-10-289-454-26	Sequence 26, App1
37	655	98.6	132	14	US-10-050-902-259	Sequence 259, App
38	655	98.6	132	14	US-10-050-898-259	Sequence 259, App
39	655	98.6	132	14	US-10-346-190-26	Sequence 26, App1
40	655	98.6	132	15	US-10-465-811-17	Sequence 17, App1
41	655	98.6	132	15	US-10-289-456-26	Sequence 26, App1
42	655	98.6	132	15	US-10-622-064-9	Sequence 9, App1
43	655	98.6	132	15	US-10-622-124-20	Sequence 20, App1
44	655	98.6	132	16	US-10-622-087-20	Sequence 20, App1
45	652	98.2	132	14	US-10-243-739-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-10-243-739-25
; Sequence 25, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornio, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243, 739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318, 967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-25

Query Match	100.0%	Score 664;	DB 14;	Length 132;
Best Local Similarity	100.0%	Pred. No. 2.1e-66;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ARLETTYLGNIGRDGKQTLVLPNGVNPNGVNLGASLSQAGAVPLERKVVTVSVSQPSRNK 60		
DB	1	ARLETTYLGNIGRDGKQTLVLPNGVNPNGVNLGASLSQAGAVPLERKVVTVSVSQPSRNK 60		
QY	61	NYVQVQKIONPACTANGSCDSVTRQKADYVTFSTQXSTDEERAFVTELAALASPL 120		
DB	61	NYVQVQKIONPACTANGSCDSVTRQKADYVTFSTQXSTDEERAFVTELAALASPL 120		
QY	121	LDAIDQINPAY 132		

Db 121 LIDAIQDLPAY 132

RESULT 2
US-10-244-065-25

/ Sequence 25, Application US/10244065
/ Publication No. US20030099668A1
/ GENERAL INFORMATION:
/ APPLICANT: Bachmann, Martin F.
/ APPLICANT: Storni, Tazio
/ APPLICANT: Maurer, Patrick
/ APPLICANT: Tisot, Alain
/ APPLICANT: Schwart, Katrin
/ APPLICANT: Meijerink, Edwin
/ APPLICANT: Lipowsky, Gerard
/ APPLICANT: Pumpens, Paul
/ APPLICANT: Cielesns, Indulis
/ APPLICANT: Renhofs, Regina
/ TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
/ FILE REFERENCE: 1700.0230001
/ CURRENT APPLICATION NUMBER: US/10/244,065
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 60/374,145
/ PRIOR FILING DATE: 2002-04-22
/ PRIOR APPLICATION NUMBER: 60/318,994
/ PRIOR FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 25
/ LENGTH: 132
/ TYPE: PRT
/ ORGANISM: Bacteriophage Q-beta
US-10-244-065-25

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETVTLGNIGRDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQPSRNK 60
DB 1 ARLETVTLGNIGRDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDBERAFVTELAALLASPL 120
DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 3
US-10-289-454-25

/ Sequence 25, Application US/10289454
/ Publication No. US20030157479A1
/ GENERAL INFORMATION:
/ APPLICANT: Bachmann, Martin
/ APPLICANT: Ueminger, Gary
/ APPLICANT: Sonderegger, Ivo
/ TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
/ FILE REFERENCE: 1700.0360001
/ CURRENT APPLICATION NUMBER: US/10/289,454
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: US 60/396,636
/ PRIOR FILING DATE: 2002-07-19
/ PRIOR APPLICATION NUMBER: PCT/IB02/00166
/ PRIOR FILING DATE: 2002-01-21
/ PRIOR APPLICATION NUMBER: US 10/050,902
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/331,045
/ PRIOR FILING DATE: 2001-11-07

/ NUMBER OF SEQ ID NOS: 386
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 25
/ LENGTH: 132
/ TYPE: PRT
/ ORGANISM: Bacteriophage Q-beta-250
US-10-289-454-25

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETVTLGNIGRDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQPSRNK 60
DB 1 ARLETVTLGNIGRDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDBERAFVTELAALLASPL 120
DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 4
US-10-050-902-257

/ Sequence 257, Application US/10050902
/ Publication No. US20030175290A1
/ GENERAL INFORMATION:
/ APPLICANT: Renner, Wolfgang A.
/ APPLICANT: Bachmann, Martin
/ APPLICANT: Tisot, Alain
/ APPLICANT: Maurer, Patrick
/ APPLICANT: Lechner, Franziska
/ APPLICANT: Seibel, Peter
/ APPLICANT: Plosek, Christine
/ TITLE OF INVENTION: Molecular Antigen Array
/ FILE REFERENCE: 1700.0190004
/ CURRENT APPLICATION NUMBER: US/10/050,902
/ CURRENT FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/262,379
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: US 60/288,549
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/326,998
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: US 60/331,045
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 350
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 257
/ LENGTH: 132
/ TYPE: PRT
/ ORGANISM: Qb 250
US-10-050-902-257

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLETVTLGNIGRDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQPSRNK 60
DB 1 ARLETVTLGNIGRDGKQTLVLPNGVPTNGVASISQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDBERAFVTELAALLASPL 120
DB 61 NYKVQYKIONPTACTANGSCDPSVTRQKYADVTFSFTQYSTDBERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 5
US-10-050-898-257
; Sequence 257, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tiseet, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plosek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staudenfel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 257
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 250
US-10-050-898-257

Query Match
Best Local Similarity 100.0%; Score 664; DB 14; Length 132;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 1 ARLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

Qy 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALASPL 120
Db 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALASPL 120

Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 6
US-10-346-190-25
; Sequence 25, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 250
US-10-346-190-25

Query Match
Best Local Similarity 100.0%; Score 664; DB 14; Length 132;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 1 ARLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

Qy 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALASPL 120
Db 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALASPL 120

Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 7
US-10-465-811-16
; Sequence 16, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 16
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
US-10-465-811-16

Query Match
Best Local Similarity 100.0%; Score 664; DB 15; Length 132;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 1 ARLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

Qy 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALASPL 120
Db 61 NYKVQKIONPTACTANGSCDPSVTROKADVTFSFTQYSTDEBERAFVTELAALASPL 120

Qy 121 LIDAIDQLNPAY 132
Db 121 LIDAIDQLNPAY 132

RESULT 8
US-10-289-456-25
; Sequence 25, Application US/10289456

```

PublicatIon No. US2004003321A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
PRIORITY FILING DATE: 2002-11-07
PRIORITY APPLICATION NUMBER: PCT/IB02/00166
PRIORITY FILING DATE: 2002-01-21
PRIORITY APPLICATION NUMBER: US 10/050,902
PRIORITY FILING DATE: 2002-01-18
PRIORITY APPLICATION NUMBER: US 60/396,635
PRIORITY FILING DATE: 2002-07-19
PRIORITY APPLICATION NUMBER: US 60/331,045
PRIORITY FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Q-beta 250 mutant
US-10-289-456-25

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Query Match	100.0%;	Score 664;	DB 15;	length 132;
Best Local Similarity	100.0%;	Pred. No. 2,1e-66;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ARLEVTVLGNIGRDOKQTLVLPNPGVNPPTNGVASLSQGAAPALAEKRVTVSVSOPSRNRK	60	
Db	1	ARLEVTVLGNIGRDOKQTLVLPNPGVNPPTNGVASLSQGAAPALAEKRVTVSVSOPSRNRK	60	
QY	61	NYKQVQKIQNPFTACPNANGSCDPSVTRQKADVTFSFTQYSDDEBAFRTETLAALLASPL	120	
Db	61	NYKQVQKIQNPFTACPNANGSCDPSVTRQKADVTFSFTQYSDDEBAFRTETLAALLASPL	120	
QY	121	LIDAIIDQLNPAY	132	
Db	121	LIDAIIDQLNPAY	132	

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RESULT 9
US-10-622-064-8
; Sequence 8, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurel, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.030001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 132
; TYPE: PRNT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
; US-10-622-064-8

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```
Query Match          100.0%; Score 664; DB 15; length 132;  
Best Local Similarity 100.0%; Pred. No. 2.1e-66;  
Matches 132; Conservative 0; Mismatches 0; Indels 0  
  
QY      1 ARLEVTITGNTGRDGKQTIVLPNGVNPINGVASLSQAQAVPALERKTVVSVSQSPRRNK 60  
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[illegible]

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1 RESULT 10
2 US-10-622-124-19
3 Sequence 19, Application US/10622124
4 Publication No. US20040076645A1
5 GENERAL INFORMATION:
6 APPLICANT: Bachmann, Martin F
7 APPLICANT: Pulurijs, Alma
8 TITLE OF INVENTION: Ghrelin-Carrier Conjugates
9 FILE REFERENCE: 1700.0340001
10 CURRENT APPLICATION NUMBER: US/10/622,124
11 CURRENT FILING DATE: 2003-07-18
12 PRIOR APPLICATION NUMBER: US 60/396,638
13 PRIOR FILING DATE: 2002-07-19
14 NUMBER OF SEQ ID NOS: 146
15 SOFTWARE: PatentIn version 3.2
16 SEQ ID NO 19
17 LENGTH: 132
18 TYPE: PR1
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
22 US-10-622-124-19

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Query March	100.0%;	Score 664;	DB 15;	Length 132;
Best Local Similarity	100.0%;	Pred. No. 2,1e-66;		
Matches 133;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ARLETVTLGNIGRGDKQTLVILNPRGVNPTNGVASISQAGAVPALEKRYTVSVSOPSRRNK	60	
Db	1	ARLETVTLGNIGRGDKQTLVILNPRGVNPTNGVASISQAGAVPALEKRYTVSVSOPSRRNK	60	
QY	61	NYKYQYKIQNPRACTNGSCDPSVTRKQKADVTFSFTQSYTNDERBAFVRETLAALLSPL	120	
Db	61	NYKYQYKIQNPRACTNGSCDPSVTRKQKADVTFSFTQSYTDERBAFVRETLAALLSPL	120	
QY	121	LIDAIDQLNPAY	132	
Db	121	LIDAIDQLNPAY	132	

```

, RESULT 11
, US-10-622-087-19
, Sequence 19, Application US/10622087
, Publication No. US20040141984A1
, GENERAL INFORMATION:
, APPLICANT: Bachmann, Martin F
, APPLICANT: Tisoc, Alain
, APPLICANT: Ortman, Rainer
, APPLICANT: Luond, Rainer
, APPLICANT: Staufenbiel, Matthias
, APPLICANT: Frey, Peter
, TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
, FILE REFERENCE: 1700.035002
, CURRENT APPLICATION NUMBER: US/10/622,087
, CURRENT FILING DATE: 2003-07-18
, PRIOR APPLICATION NUMBER: US 60/396,639
, PRIOR FILING DATE: 2002-07-19
, PRIOR APPLICATION NUMBER: US 60/470,432
, PRIOR FILING DATE: 2003-05-15
, NUMBER OF SEQ ID NOS: 93
, SOFTWARE: PatentIn version 3.2
, SEQ ID NO 19

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LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 250 mutant
US-10-622-087-19

Query Match 100.0%; Score 664; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 2, 1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
DB 1 ARLEVTTLGNIGDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
QY 61 NYKVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 12
US-10-243-739-23
Sequence 23, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornl, Tazio
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-23

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4, 5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
DB 1 ARLEVTTLGNIGDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
QY 61 NYKVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 13
US-10-244-065-23
Sequence 23, Application US/10244065
Publication No. US2003009668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornl, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tisot, Alain

APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Clejens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-23

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4, 5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
DB 1 ARLEVTTLGNIGDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60
QY 61 NYKVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQKIQNPACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIQDLPAY 132
DB 121 LIDAIQDLPAY 132

RESULT 14
US-10-289-454-23
Sequence 23, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-240
US-10-289-454-23

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4, 5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSNRK 60

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Db      1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVSLSQAGAVPALKKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPFTACTANGSCDPSVTRQKADVTFSSFTQYSTDERAFVRTETLAALLASPL 120
Db      61 NYKVQVKIQNPFTACTANGSCDPSVTRQKADVTFSSFTQYSTDERAFVRTETLAALLASPL 120
QY      121 LIDAIQOLNPAY 132
Db      121 LIDAIQOLNPAY 132
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RESULT 15

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US-10-050-902-255
; Sequence 255, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 132
; TYPE: PRT
; ORGANISM: QB 240
US-10-050-902-255
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Query Match      99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ARLETVTLGNIGRDGKQTLVLPNGVNPPTNGVSLSQAGAVPALKKRVTVSVSQPSNRK 60
Db      1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVSLSQAGAVPALKKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPFTACTANGSCDPSVTRQKADVTFSSFTQYSTDERAFVRTETLAALLASPL 120
Db      61 NYKVQVKIQNPFTACTANGSCDPSVTRQKADVTFSSFTQYSTDERAFVRTETLAALLASPL 120
QY      121 LIDAIQOLNPAY 132
Db      121 LIDAIQOLNPAY 132
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Search completed: January 4, 2005, 09:41:22
Job time : 32.7351 secs

C:Accession: S01964
C:Inokuchi, Y.; Jacobson, A. B.; Hirose, T.; Inayama, S.; Hirashima, A.
Nucleic Acids Res. 16, 6205-6221, 1988
A:Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP
A:Reference number: S01963; MUID:88289362; PMID:339390
A:Accession: S01964
A:Status: Preliminary
A:Molecule type: genomic RNA
A:Residues: 1-331 <INO>
A:Cross-references: UNIPROT:P09677; EMBL:X07489
A:Note: the authors translated the readthrough stopcodon TGA for residue 133 as Trp
A:Superfamily: phage GA coat protein

Query Match 79.3%; Score 526.5; DB 2; Length 331;
Best Local Similarity 77.3%; Pred. No. 3.5e-44;
Matches 102; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

QY 1 ARLEVTTLGNIGRDEKQTLLVLPNGVPNTNGVASISAGAAVPALKEKRVTSVSOPSSNRNK 60
::|::|::|:
2 AKNQVTLTKSKIKGKGDDQTLLTPRGVNPTNGVASISEKAAPPALEKRTVTSVAQPSRRNK 61

Db

QY 61 NYKYQVKIQNFCTANGSCDPSVTRQCKADVTSTFTSYSDERAFPRTELAAILASPL 120
::|::|::|::|:
62 NFKVOIKIQNFCTACRD-ACDPVSYRSFAFADVLTSTFSYSDBERALTRETAAILADPL 120

Db

QY 121 LIDAIIDLNPAY 132
::|::|::|::|
Db 121 IVDAILDNLPAY 132

```

RESULT 3
VCBPPI
coat protein - phage PRRI
C:Species: phage PRRI
C:Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C:Accession: A04225
R:Daesele, P./ Vandekerckhove, J.S.; Van Montagu, M.C.
Eur. J. Biochem. 94, 375-386, 1979
A:Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage PRRI
A:Reference number: A04225; MUID:79148387; PMID:107028
A:Accession: A04225
A:Molecule type: protein
A:Residues: 1-131 <DHA>
A:Cross-references: UNIPROT:P03616
A:Superfamily: phage GA coat protein

```

```

Query Match      17.5%; Score 116; DB 1; Length 131;
Best Local Similarity 33.3%; Pred. No. 0.00031;
Matches 42; Conservative 14; Mismatches 50; Indels 16; Gaps 5;

QY 17 QTVLNLPRGVNPT-----NGVASLSQAGAVPALEKEVTVSQSPSHRNKRYKQV 66
Db 4 QNVLLKDRERAPNDHTFVPRDIRNNGVEVESTGVPIDIESFTLSRKTSGNR--YKSTL 61

QY 67 KIQNPVT--ACTANGSCDPSVTRQKIADVTSESFTQYSTDDEER-APYRETLALLASPLLI- 122
Db 62 KLVPVVSQSTVNGIIVTPVVVRTSVTVFDYDARSTKEKNFVGMIADALKADLMIVH 121

QY 123 DAIDQLNPAY 132
Db 122 DTIVNLQGVY 131

```

```

RESULT 4
S22340
seeligeriolysin - Listeria seeligeri
C:Species: Listeria seeligeri
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: S22340
R:Haas, A.; Dumbsky, M.; Krefl, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A:Title: Listeria lysin genes: complete sequence of ilo from Listeria ivanovi and of lsc
#:Reference number: S22340; MUID:92182018; PMID:1543752

```

A:Accession: S22340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <HA>
A:Cross-references: UNIPROT:P31830, EMBL:X60462, NID:g44144, PIDD:CAA2996.1, PTD:g44145
A:Note: the authors translated the codon GCC for residue 287 as Pro
!Superfamily: dipeptide transport protein

Query Match	13.2%	Score 87.5;	DB 2;	Length 530;
Best Local Similarity	24.3%	Pred. No. 1;		
Matches	33;	Conservative	23;	Mismatches 37;
			Indels	43;
			Gaps	7;

QY	13	RDKQÖTLVL--NPRGVNPT-----	NGVASLSQAGA-----	VPALKERV	48
		: : : : : : : : : : : :	: : : : : : : : :	:	
Db	94	KDGEISYIVVEKKKGINQNNADISVINASISLTYPGALVKANRELVENQPNVLVPRDSTL			153
QY	49	TVTSVGSÖSSRRKRNKRYKVQKIONPFACTIANGSCDPSVYR--QKY-----		ADVTFSPTQ	98
		: : : : : : : : : : : :	: : : : : : : : : :	:	
Db	154	TLSDVLDTGKMTKKDKKIFVK--NPTKSNVNNAVNVLTVLRMNDKYSKAYPNINAKIDYS--			208
QY	99	YSTDEERAPFVRTLELAA			114
		: : : : : : : : : :	: : : : : : : : : :	:	
Db	209	----DEMAYISEÖLTA			220

RESULT 5

T00646
hypothetical protein F316.9 - *Arabidopsis thaliana*
C|Species: *Arabidopsis thaliana* (mouse-ear cress)
C|Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #ext_change 09-Jul-2004
C|Accession: T00646
R|Fetzerpietl, N.A.; Palm, C.J.; Conway, A.B.; Kutz, D.B.; Conway, A.R.; Au, M.; Araujo,
I.; Vysotskaya, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, February 1998
A|Reference number: Z14197
A|Accession: T00646
A|Status: translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-540 <FED>
A|Cross-references: UNIPROT:O48683; EMBL:AC002396; NID:Z2749218; PIDN:AA00577.1; PID:g28
C|Genetic:1
A|Gene: AT5G.F316.9
A|Map position: 1
A|Intons: 14/3, 281/3, 428/3, 448/2, 483/3, 502/3
A|Superfamily: pyruvate dehydrogenase (lipamide) alpha chain; thiamin pyrophosphate-bind

```

QY      11  IGRNKTGLVLPNG--VNPTNGVATLSQAGNPALEKRYTVSVSPRRNRK-YKQV 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     255  VKKEKKNLLKQDGNVRIINPTKSLKPNQGVGKPEIRNKTVTSKTPSKMKMMKATIK 314
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      67  KIQNPACTANGSCDPSVTRKQADVTFTSTQYSTDEBRAVFTTEALATLAPLL 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     315  KPAAPMSKSQGGAFPRVYRKPAPTKLTLSHSLKKEK-----VSPILL 358
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 6
S24231
1,18-eriololysin precursor - Listeria monocytogenes (strain 12067)
C/Species: Listeria monocytogenes
A/Variety: strain 12067
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #ext_change 09-Jul-2004
C/Accession: S24231
R/Rasmussen, O.F.; Beck, T.; Olsen, J.E.; Dons, L.; Rossen, L.
Infect. Immun. 59, 3945-3951, 1991
A>Title: Listeria monocytogenes isolates can be classified into two major types according
A/Reference number: S24230; PMID:92040062; PMID:1937753
A/Accession: S24231
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

```


A/Residues: 1-529 <RAS>
A/Cross-references: UNIPROT:P13128; EMBL:X60035; NID:G44110; PIDN:CAA42639.1; PID:G44112
A/Experimental source: strain 12067, serotype 4b
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C/Genetics:
A/Gene: hlyA
C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-529/Product: listeriolysin #status predicted <Mat>

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLV-----NPRGVNPTNGVASLSQGA-----VPALEKRV 48
DB 93 KQGENETIVEKKKKKSIQNNADIQVNNALISLTYPALVKANSELVENQDVLVPRRDSL 152
QY 49 TVSVSQPSHRNRKRYQVQKIQNPACTANGSCDPSVTR-----QKYADVTFSTGYSTD 102
DB 153 TISIDLPGMTNDQNKIVK--NATKSNVNNAVNTLVERNNEKKAQAYPRVVS---AKIDYD 207

QY 103 EERAFVETELAA 114
DB 208 DEMAYSESQLIA 219

RESULT 7
A/3505
Listeriolysin O precursor - Listeria monocytogenes
C/Species: Listeria monocytogenes
C/Date: 21-Oct-1992 #sequence revision 21-Oct-1992 #text_change 09-Jul-2004
C/Accession: A43505; S05306; A47606; S12400; A61079
R/Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Glacquel-Sanrey
Interf. Immun. 56, 766-772, 1988
A/Title: Expression in *Escherichia coli* and sequence analysis of the listeriolysin O de
A/Reference number: A43505; MUID:88153053; PMID:3126142
A/Accession: A43505
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <MEN>
A/Cross-references: UNIPROT:P13128; GB:M24199; NID:G149652; PIDN:AAA03018.1; PID:G149653
A/Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
Nucleic Acids Res. 17, 6406, 1989
R/Domain, E.; Chakraborty, T.
A/Title: Nucleotide sequence of the listeriolysin gene from a *Listeria monocytogenes* ser
A/Reference number: S05306; MUID:89366684; PMID:2505236
A/Accession: S05306
A/Molecule type: DNA
A/Residues: 1-529 <DOM>
A/Cross-references: EMBL:X15127; NID:G44106; PIDN:CAA33223.1; PID:G44107
A/Experimental source: strain EGD
A/Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R/Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cossart, P.
Infect. Immun. 55, 3225-3227, 1987
A/Title: Identification of the structural gene encoding the SH-activated hemolysin of *L*
A/Reference number: A47606; MUID:88057627; PMID:2824384
A/Accession: A47606
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 413-480 <ME2>
A/Cross-references: GB:M29171
R/Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A/Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtain
A/Reference number: S12400; MUID:91311627; PMID:1965218
A/Accession: S12400
A/Molecule type: DNA
A/Residues: 483-493 <MTC>
A/Experimental source: strain LO28, serotype 1/2c
C/Genetics:
A/Gene: hlyA, hlyA

C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-529/Product: listeriolysin O #status predicted <Mat>

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLV-----NPRGVNPTNGVASLSQGA-----VPALEKRV 48
DB 93 KQGENETIVEKKKKKSIQNNADIQVNNALISLTYPALVKANSELVENQDVLVPRRDSL 152
QY 49 TVSVSQPSHRNRKRYQVQKIQNPACTANGSCDPSVTR-----QKYADVTFSTGYSTD 102
DB 153 TISIDLPGMTNDQNKIVK--NATKSNVNNAVNTLVERNNEKKAQAYPRVVS---AKIDYD 207

QY 103 EERAFVETELAA 114
DB 208 DEMAYSESQLIA 219

RESULT 8
AC1100
Listeriolysin O precursor [imported] - Listeria monocytogenes (strain EGD-e)
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC1100
R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Blocker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Feihl, H.;
Science 294, 849-852, 2001
D.; Jones, L.M.; Karst, U.
A/Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A/Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1100
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <GLA>
A/Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:G16409567; GSPDB:C
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: hly
C/Superfamily: dipeptide transport protein

Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLV-----NPRGVNPTNGVASLSQGA-----VPALEKRV 48
DB 93 KQGENETIVEKKKKKSIQNNADIQVNNALISLTYPALVKANSELVENQDVLVPRRDSL 152
QY 49 TVSVSQPSHRNRKRYQVQKIQNPACTANGSCDPSVTR-----QKYADVTFSTGYSTD 102
DB 153 TISIDLPGMTNDQNKIVK--NATKSNVNNAVNTLVERNNEKKAQAYPRVVS---AKIDYD 207

QY 103 EERAFVETELAA 114
DB 208 DEMAYSESQLIA 219

RESULT 9
S57537
MKT1 protein - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein N2302; protein YNL085w
C/Species: *Saccharomyces cerevisiae*
C/Date: 10-Oct-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S57537; S50279; S63024; S63017; S65096
R/Soler-Mita, A.; Saitz, J.E.; Balilesta, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A/Reference number: S57533

A:Accession: S57537
A:Molecule type: DNA
A:Residues: 1-830 <SOL>
A:Cross-references: UNIPROT:P40850, EMBL:X89016, NID:g887621, PID:g887626
R:Vermut, M.; Widner, W.R.; Dimman, J.D.; Wickner, R.B.
Yeast 10, 1477-1479, 1994
A:Title: Sequence of MKT1, needed for propagation of M(2) satellite dsRNA of the I-A virus
A:Reference number: S50279, MUID:95176705, PMID:7532890
A:Accession: S50279
A:Molecule type: DNA
A:Residues: 1-29, 'G', 31-808, 'TMKTCINHH' <VER>
A:Cross-references: EMBL:U05123, NID:G520475, PIDN:AA649470.1, PID:G520476
R:Solier-Mita, A.; Saliz, J.E.; Ballesta, J.P.G.; Remacha, M.
Submitted to the Protein Sequence Database, April 1996
A:Reference number: S63018
A:Accession: S63024
A:Molecule type: DNA
A:Residues: 1-830 <SOM>
A:Cross-references: EMBL:Z71361, NID:G1301982, PID:G1301983, MIPS:YNL085W
A:Experimental source: Strain S28C
R:Poehlmann, R.; Philippse, P.
Submitted to the Protein Sequence Database, April 1996
A:Reference number: S62997
A:Accession: S63017
A:Molecule type: DNA
A:Residues: 569-830 <POE>
A:Cross-references: EMBL:Z71361, MIPS:YNL085W
A:Experimental source: Strain S28C
R:Solier-Mita, A.; Saliz, J.E.; Ballesta, J.P.G.; Remacha, M.
Yeast 12, 485-491, 1996
A:Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
A:Reference number: S65092, MUID:96310626, PMID:8740422
A:Accession: S65096
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-830 <SOF>
A:Cross-references: EMBL:X89016, NID:g887621, PIDN:CAA61425.1, PID:g887626
C:GeneticB:
A:Gene: SGD:MKT1
A:Cross-references: SGD:S0005029, MIPS:YNL085W
A:Map position: 14L
C:Superfamily: Saccharomyces cerevisiae MKT1 protein
C:Keywords: transmembrane protein
F:615-631/Domain: transmembrane #stratus predicted <TM>

Query Match 12.2%, Score 81, DB 2, Length 830,
Best Local Similarity 25.7%, Pred. No. 7.5,
Matches 26, Conservative 20, Mismatches 49, Indels 6, Gaps 3;

OY 5 TTTTGGTGRDQKQTLVTPRGVNPFTNGVASSQAGVALEKRTVSQPSRRKRYKV 64
DB 301 STTIGN--DKENIGNQKRGISALRYMPVUKDQKQKELFVQELIVSBEDEKKNKDGK- 356

OY 65 QVKIQNPACTANGSCDPSVTRQKYADVTFSFTQYSTDDEER 105
DB 357 KSNLSSPS--SASSASASPATVTYTKNASSEKLTYESKSTVEVR 395

RESULT 10
KGBYH1
CYC1/CY3 transcription activator - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein I9672.1, protein YLR556w, regulatory protein CYP1, regulatory protein CYP1;
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1991 #sequence revision 23-Feb-1996 #text_change 12-Nov-1999
A:Accession: S59400, A31312, S15447, S05804, S15446
R:Johnson, D.
Submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9672.
A:Reference number: S59386
A:Accession: S59400
A:Molecule type: DNA
A:Residues: 1-1502 <JOH>
A:Cross-references: EMBL:U20865, NID:g662330, PIDN:AA867387.1, PID:g662331, GSPDB:GN00001

[illegible]

A:Gene: 110
 C:Superfamily: dipeptide transpore protein
 F:1-24/Domain: signal sequence <Status predicted <Sig-
 F:25-528/Product: 1vanolysin #status predicted <Mnt>

Query Match 11.7%; Score 77.5; DB 2; Length 528;
 Best Local Similarity 21.2%; Pred. No. 9.8;

Matches 28; Conservative 25; Mismatches 44; Indels 35; Gaps 5;

QY 13 RGGKQNLV-----NPRGVNPTNGVASLSQAG-----VPALEKRY 48
 DB 92 KCGNQITVEKKKKKSIQNNADIQVINSLASTYPPALVANSSELVENQDVLPRDSV 151
 QY 49 TVSVSQPSRRKKYKQVQKIQNPTACTANGSCDPSYTR-----QKXADVTFSFTQYSTD 102
 DB 152 TISIDLP--GMVNHDEIVQVQNTKSNINDGVTLVDRMNNKSEEPNLS---AKIDVD 206
 QY 103 EERAFVETELAA 114
 DB 207 QEMAYSESQLV 218

RESULT 12

TJ1660
 hypothetical protein COS41.6 - sea equit (Clona intestinalis)

C:Species: Clona intestinalis

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: TJ1660

R:Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Dobson, R.; Tweedie, S.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z21049

A/Accession: TJ1660

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-432 <RIR>

A/Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDN:CAB0605

C:Genetics:

A:introns: 180/2; 212/1; 229/3

Query Match 11.6%; Score 77; DB 2; Length 432;
 Best Local Similarity 27.4%; Pred. No. 8.7;

Matches 31; Conservative 17; Mismatches 47; Indels 18; Gaps 6;

QY 4 ETVTLLNIGRDGKQTLVLPNGVNPNGVASLSQAGVPALEKRYTVSVSQPSRRKKY 63
 DB 242 DTSSEGEVTKDGGNLAENP---TPSNARELOESVASVLETTVYKSAIQ--EQDSSAIR 257
 QY 64 VQVKIQNPACTA-----NGSCDPSVTRQKADVTFSF--TOYSTDE 103
 DB 298 KE-NPQNAACPFRNGNCVSTNSNKTNPDSKIEIVNSDNTDEDTQIDITNE 349

RESULT 13

C98221
 hypothetical protein AGR_L_1428 [imported] - Agrobacterium tumefaciens (strain C58, Cerc

C/Species: Agrobacterium tumefaciens

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C/Accession: C98221

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Woliam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2333-2328, 2001

A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A/Reference number: A97359; WUID:21608551; PMID:11743194

A/Accession: C98221

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <RUR>

A/Cross-references: UNIPROT:Q8U8F3; GB:AE007870; PIDN:AAK8293.1; PID:G15159127; GSPDB:G

C:Genetics:

A:Gene: AGR_L_1428

A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;

Best Local Similarity 24.6%; Pred. No. 2.5;
 Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGRDGKQTLVLPNGVNPNGVASLSQAGV-----PALKRYTVSVSQPSRR 59
 DB 3 ISDKGQTSADPFWHEWVTGTISTLLVAMFGWIAVDYRRSPPEARFEIAVTGVEGQT 62
 QY 60 KMYKQVQKIQNPACTA-----NGSCDPSVTRQKADVTFSF--TOYSTDEERAFVTE 111
 DB 63 GQYRVKFAIHNLSMTTAAQVNVKRGDLEQNGASPEKNADVTFDYVASSKONGTLFFRSD 120

RESULT 14

AE3065

conserved hypothetical protein Atu4139 [imported] - Agrobacterium tumefaciens (strain C58

C/Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: AE3065

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wco, L.

erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCellie

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E

ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; WUID:21608550; PMID:11743193

A/Accession: AE3065

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <RUR>

A/Cross-references: UNIPROT:Q8U8F3; GB:AE008689; PIDN:AAU44939.1; PID:G17742593; GSPDB:G

A/Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu4139

A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;
 Best Local Similarity 24.6%; Pred. No. 2.5;

Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGRDGKQTLVLPNGVNPNGVASLSQAGV-----PALKRYTVSVSQPSRR 59
 DB 3 ISDKGQTSADPFWHEWVTGTISTLLVAMFGWIAVDYRRSPPEARFEIAVTGVEGQT 62
 QY 60 KMYKQVQKIQNPACTA-----NGSCDPSVTRQKADVTFSF--TOYSTDEERAFVTE 111
 DB 63 GQYRVKFAIHNLSMTTAAQVNVKRGDLEQNGASPEKNADVTFDYVASSKONGTLFFRSD 120

RESULT 15

C64221

hypothetical 114K protein (Mgpa 3' region) - Mycoplasma genitalium

C/Species: Mycoplasma genitalium

C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

C/Accession: C64221; J00092; S18702; S18703

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.J.

; C.A.; Venter, J.C.

Science 270, 397-403, 1995

A>Title: The minimal gene complement of Mycoplasma genitalium.

A/Reference number: A64200; WUID:96026346; PMID:7569993

A/Accession: C64221

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1052 <TIGR>

A/Cross-references: UNIPROT:P22747; GB:U39696; GB:L43967; NID:G1045869; PID:G1045877; TIC

A/Experimental source: strain G-37

R:Inamine, J.M.; Loechel, S.; Collier, A.M.; Barile, M.F.; Hu, P.C.

Gene 82, 259-267, 1989

A>Title: Nucleotide sequence of the Mgpa (mgp) operon of Mycoplasma genitalium and compa

A/Reference number: J00090; WUID:90060815; PMID:2583522

A/Accession: J00092

A:Molecule type: DNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-8
Perfect score: 664
Sequence: 1 ARLEVTGLGNIGRDGKQTLV.....ALLASPLILDAIDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652	98.2	133	1	COAT_BPOBE
2	652	98.2	133	2	AAM3J126
3	652	98.2	329	2	08LME1
4	652	98.2	329	2	AAL1663
5	561	84.5	133	2	09TOR9
6	561	84.5	329	2	064307
7	541	81.5	133	2	09TOS0
8	541	81.5	329	2	064303
9	526.5	79.3	132	1	COAT_BPSP
10	526.5	79.3	331	1	VAL_BPSP
11	493.5	74.3	132	2	09TOR8
12	493.5	74.3	330	2	064310
13	116	17.5	131	1	COAT_BPSP
14	96.5	14.5	473	1	08VDC2
15	87.5	13.2	530	1	TACY_LISSB
16	87.5	13.2	530	2	AAP97361
17	85.5	12.9	540	2	048683
18	82	12.3	512	2	06HGA7
19	81.5	12.3	529	1	TACY_LISSP
20	81.5	12.3	529	1	TACY_LISSP
21	81.5	12.3	529	2	09L5B9
22	81.5	12.3	529	2	06E9A2
23	81.5	12.3	529	2	06E9A2
24	81.5	12.3	529	2	06E9A2
25	81.5	12.3	529	2	06E9A2
26	81.5	12.3	529	2	06E9A2
27	81.5	12.3	529	2	06E9A2
28	81.5	12.3	529	2	06E9A2
29	81.5	12.3	529	2	06E9A2
30	81.5	12.3	529	2	06E9A2
31	81.5	12.3	529	2	06E9A2

32	81.5	12.3	529	2	AAT03000	AAT03000 listeria
33	81	12.2	325	2	Q73R79	Q73R79 treponema d
34	81	12.2	325	2	AAS10709	AAS10709 treponema
35	81	12.2	830	1	MKT1 YEAST	P40650 saccharomyc
36	81	12.2	830	2	08TF87	08TF87 saccharomyc
37	81	12.2	830	2	08TF89	08TF89 saccharomyc
38	81	12.2	830	2	08TF85	08TF85 saccharomyc
39	81	12.2	830	2	08TF85	08TF85 saccharomyc
40	81	12.2	830	2	08TF85	08TF85 saccharomyc
41	81	12.2	830	2	AAM00519	AAM00519 saccharom
42	81	12.2	1624	2	09Y3K8	09Y3K8 drosophila
43	81	12.2	1637	2	09Y3K8	09Y3K8 drosophila
44	80.5	12.1	1502	1	CYPI YEAST	P12351 saccharomyc
45	79.5	12.0	608	2	084H79	084H79 rhodococcus

ALIGNMENTS

RESULT 1
ID COAT_BPOBE STANDARD; PRT; 132 AA.
AC P03615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coar protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirginis.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clemons I., Dreilima D., Dislers A., Baumanis V.,
Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmis C., Sastre P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
bacteriophage Q-beta as an application of a mapping procedure for RNA
fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Meite T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmhamadi R., Fridborg K., Bunde M., Vaiegard K., Lilljas L.;
RT "Structure of bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
CC -!- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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CC EMBL; M99039; AAA16662.1; -
 CC EMBL; V00643; CAA33992.1; -
 DR PIR; A92240; VCBPOB.
 DR PDB; 1QBE; X-ray; A/B/C=1-132.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
 FT INIT MET 0 0
 FT CONFLICT 22 22 N -> D (in Ref. 4).
 FT CONFLICT 56 56 Missing (in Ref. 4).
 FT STRAND 6 9
 FT TURN 13 14
 FT TURN 18 27
 FT TURN 28 31
 FT STRAND 32 36
 FT HELIX 42 44
 FT STRAND 47 53
 FT STRAND 56 56
 FT TURN 57 58
 FT STRAND 59 59
 FT STRAND 62 74
 FT STRAND 83 96
 FT TURN 98 99
 FT HELIX 102 117
 FT HELIX 119 126
 FT TURN 127 127
 SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA572E CRC64;

Query Match 98.2%; Score 652; DB 1; Length 132;
 Best Local Similarity 97.7%; Pred. No. 1.3e-55;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 AKLEVTTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 RESULT 2
 ID AAM33126 PRELIMINARY; PRT; 133 AA.
 AC AAM33126.
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Coat protein.
 OS Bacteriophage Q-beta.
 OS viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alilelevivirus; Alilelevivirus subgroup III.
 OX NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Bacher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes.";
 RL BMC Evol. Biol. 3:24-24(2003).
 DR EMBL; AY099114; AAM33126.1; -
 KW Coat protein.
 SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.2%; Score 652; DB 2; Length 133;
 Best Local Similarity 97.7%; Pred. No. 1.4e-55;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 2 AKLEVTTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 61
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 121
 QY 121 LIDAIDQLNPAY 132
 DB 122 LIDAIDQLNPAY 133

RESULT 3
 ID Q8LTEL1 PRELIMINARY; PRT; 329 AA.
 AC Q8LTEL1.
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE A1 read-through protein (A1 protein).
 OS Bacteriophage Q-beta.
 OS viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alilelevivirus.
 OX NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Bacher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes.";
 RL BMC Evol. Biol. 3:24-24(2003).
 SQ SEQUENCE FROM N.A.
 RP MEDLINE=94109687; PubMed=7506687;
 RX Kozlovskaya T.M., Clelens I., Drellima D., Dieters A., Baumann V.,
 RA Ose V., Pumpens P.;
 RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
 assembled in Escherichia coli.";
 RL Gene 137:133-137(1993).
 DR EMBL; AY099114; AAM33127.1; -
 DR EMBL; M99039; AAA16663.1; -
 DR HSP; P03615; IQBE.
 DR GO; GO:0019028; C:virol capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1_coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.2%; Score 652; DB 2; Length 329;
 Best Local Similarity 97.7%; Pred. No. 3.9e-55;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 2 AKLEVTTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 61
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 120
 DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVTELAALLASPL 121
 QY 121 LIDAIDQLNPAY 132
 DB 122 LIDAIDQLNPAY 133

RESULT 4
 ID AAA16663 PRELIMINARY; PRT; 329 AA.
 AC AAA16663.
 DT 02-MAR-2004 (TReMBLrel. 27, Created)

DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DS A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolevivirus.
OX NCBI_TaxId=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94103687; PubMed=7506687;
RA Kozlovskaya T.M., Cletens I., Dreilima D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.,
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.",
RT Gene 137:133-137(1993).
DR EMBL, M99039: AAA16663.1; -
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match	98.2%	Score	652	DB 2	Length	329
Best Local Similarity	97.7%	Pred. No.	3.9e-55			
Matches 129	Conservative	2	Mismatches	1	Indels	0
					Gaps	0

Qy	1	ARLEVTVLGNIGRCDKQTLVLPFRVNPFTNGVASLSQKGAVALPKRVTVASVQSSRRK	60
Db	2	AKLEFVTLGNIGKDKQTLVLPFRVNPFTNGVASLSQKGAVALPKRVTVASVQSSRRK	61
Qy	61	MYKXQVKRQNTACTANGSCDPSVTRKCAVDVTSFQYSTDERAFVRIETLALLASPL	120
Db	62	MYKQVKKQNTACTANGSCDPSVTRKAYADVTSFQISTDERAFVRIETLALLASPL	121
Qy	121	LIDAIIDQLNPAY	132
Db	122	LIDAIIDQLNPAY	133

RESULT 5	
Q9TOR9	
ID Q9TOR9	PRELIMINARY; PRT; 133 AA

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Major coat protein.
 OS Enterobacteriella phage MX1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allovirgavirus.
 NCBI_TaxID=75723;

RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RL J. Mol. Biol. 256:8-19(1996).

RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duijn J.
RL Submitted (APR1998) to the EMBL/GenBank/DBJ databases
RL EMBL; AF059245; AAC14699.1; -
DR HSSP; P03615; IOBE.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0005189; P: structural molecule activity; IEA.
DR InterPro; IPR002703; Dev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
KW SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;

Query Match	84.5%	Score	561	DB	2	Length	133
Best Local Similarity	81.8%	Pred. No.	1e-46				
Matches	108	Conservative	12	Mismatches	12	Indels	0
						Gaps	0

Qy	1	ARLETVLIGNRGRCOKTLYLNPGRVNPPTNGVSLQAGAVPALEKRVTVSVSPSNRK	60
Db	2	AKQATILISGIGKNDVTLINLNPGRVNPPTNGVSLQAGAVPALEKRVTVSVSPSNRK	61
Qy	61	NYKQVAKIIONPACTANGSCDPSVTRQKRVADVTPSFQYSTDEBERAFVTRTELALLPL	120
Db	62	NYKQVAKIQNPTSCTAGSTCDPSVTRSAVADVTPSFQYSTDEBERALVTELKALLDPM	121
Qy	121	LIDAIDQLNPAY	132
Db	122	LIDAIDNLNPAY	133

RESULT	6
064307	
ID	064307
AC	064307;
DT	01-AUG-1998 (TREMBLrel, 07, Created)
DT	01-AUG-1998 (TREMBLrel, 07, Last sequence update)
DT	01-MAR-2004 (TREMBLrel, 26, Last annotation update)
DE	A1-protein.
OS	Enterobacteria phage MX1.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC	Allolevivirus.
NCBI_TaxID=75723;	
NCBI_TaxID=75723;	

RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beckwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q, beta."
RJ J. Mol. Biol. 247:903-917 (1995).
RL
RN [2]

RX MEDLINE=96190948; Pubmed=8609616;
RA Beekwilder J., Nieuwenhuijsen R., Poort R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA
RL Control of A-protein synthesis.";
J. Mol. Biol. 256:8-19(1996).
[3]

RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases
DR EMBL; AF059242; AAC14700.1; --
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPRO02703; Leyt cat.
DR InterPro; IPRO00504; RNA_rec_mot.
DR Pfam; PF01819; Leyt_cat; 1.
DR PROSITE; PS00030; RRM_NDN_1; UNKNOWN_1.
SQ SEQUENCE 329 AA; 35880 MW; 37B1DD50DB52F15 CRC64;

Query Match	84.5%	Score 561;	DB 2;	Length 329;
Best Local Similarity	81.8%	Pred. No. 2.9e-46;		
Matches 108;	Conservative 12;	Mismatches 12;	Indels 0;	Gaps 0;

OY	1	ARLEVTJLGNIGRDOCKQTLVYNPRGVNPTNGVASLSQAGAVALEKRVTVSOSQPSRNK	60
Dd	2	AKLGAITISGICKNQDVTILNINPGRVNPTNGVAALSEAGAVALEKRVTVISVSQPSRNK	61
OY	61	NYKVQVKONFTACANGSCDPSTVRKQADVTFSFTOYSTDEBRAPFVNTTEIALLASPL	120
Dd	62	NYKVQVKQNFTSCNASGTCDPSTVRSAAYDVTFSTOTSTDEBRALVTELKALLADRM	121
OY	121	LIDAIQDINPAY	132
Dd	122	LIDAIQDINLPAY	133

```

RESULT 7
Q9T0S0 PRELIMINARY; PRT; 133 AA.
ID 09T0S0
AC 09T0S0
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Coat protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus.
NCBI_TaxID=74336;
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96190948; PubMed=8609616;
RX Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR Coat protein.
KM SEQUENCE 133 AA; 14198 MW; 098722E3C6CA255 CRC64;
SQ
Query Match 81.5%; Score 541; DB 2; Length 133;
Best Local Similarity 78.8%; Pred. No. 9e-45;
Matches 104; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
QY 1 ARLEVTYLTGNIGRDKQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNRK 60
DB 2 AKLQATITLSGIGKGGVTLIDLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNRK 61
QY 61 NYKVQVKIQNPCTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALLASPL 120
DB 62 NYKVQVKIQNPCTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALLADPM 121
QY 121 LIDAIIDQINPAY 132
DB 122 LVNAIDNINPAY 133
RESULT 8
ID 064303 PRELIMINARY; PRT; 329 AA.
AC 064303
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus.
NCBI_TaxID=74336;
RX MEDLINE=95239761; PubMed=7723040;
SQ

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96190948; PubMed=8609616;
RX Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06251.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN.1.
DR SEQUENCE 329 AA; 35893 MW; 3E33CDB21EB625F4 CRC64;
SQ
Query Match 81.5%; Score 541; DB 2; Length 329;
Best Local Similarity 78.8%; Pred. No. 2.6e-44;
Matches 104; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
QY 1 ARLEVTYLTGNIGRDKQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNRK 60
DB 2 AKLQATITLSGIGKGGVTLIDLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRNRK 61
QY 61 NYKVQVKIQNPCTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALLASPL 120
DB 62 NYKVQVKIQNPCTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAVFTETLAALLADPM 121
QY 121 LIDAIIDQINPAY 132
DB 122 LVNAIDNINPAY 133
RESULT 9
COAT BPSP STANDARD; PRT; 132 AA.
ID COAT BPSP
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus.
NCBI_TaxID=12027;
RX MEDLINE=88289362; PubMed=3393930;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X07489; CAA30374.1; -.
DR HSSP; P03615; IQBE.

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DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein; RNA-binding.
SQ SEQUENCE 132 AA; 14129 MW; 50B1E6CC6AFOA254 CRC64;
Query Match 79.3%; Score 526.5; DB 1; Length 132;
Best Local Similarity 77.3%; Pred. No. 2.3e-43;
Matches 102; Conservative 14; Mismatches 15; Indels 1; Gaps 1;
QY 1 ARLEVTTLGNIGRDGQTLVLPNGVNPPTNGVSLSQAGVAPLAEKRVTVSOPSRRNK 60
DB 2 AKLNQVTLKIGKNGQTLTLTPRGVNPPTNGVSLSEAGVAPLAEKRVTVSVAQPSRRNK 61
QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDBERAFVTELAALLASPL 120
DB 62 NFKVQKIQNPACTCTRD-ACDPSVTRSAFADVTLSFTSYSTDBERALLITELALLADPL 120
QY 121 LIDAIQDLPAY 132
DB 121 IYDAIDNLNPAY 132
RESULT 10
VAL_BPSP STANDARD; PRT; 331 AA.
AC P09677;
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Reactthrough protein A1 [Contains: Coat protein].
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alilevivirus.
OX NCBI_Taxid=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirashina A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
collapse SP".
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The reactthrough protein A1 includes the coat
protein sequence.
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or send an email to license@sib-sib.ch).
CC EMBL; X07489; CAB37299.1; -.
DR PIR; S01964; S01964.
DR HSSP; P03615; IOBE.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
FT CHAIN 1 132 Reactthrough protein A1.
FT CHAIN 1 331 Reactthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A664284B52C6582 CRC64;
Query Match 79.3%; Score 526.5; DB 1; Length 331;
Best Local Similarity 77.3%; Pred. No. 6.8e-43;
Matches 102; Conservative 14; Mismatches 15; Indels 1; Gaps 1;
QY 1 ARLEVTTLGNIGRDGQTLVLPNGVNPPTNGVSLSQAGVAPLAEKRVTVSOPSRRNK 60
DB 2 AKLNQVTLKIGKNGQTLTLTPRGVNPPTNGVSLSEAGVAPLAEKRVTVSVAQPSRRNK 61
QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDBERAFVTELAALLASPL 120
DB 62 NFKVQKIQNPACTCTRD-ACDPSVTRSAFADVTLSFTSYSTDBERALLITELALLADPL 120
QY 121 LIDAIQDLPAY 132
DB 121 IYDAIDNLNPAY 132

DB 62 NFKVQKIQNPACTCTRD-ACDPSVTRSAFADVTLSFTSYSTDBERALLITELALLADPL 120
QY 121 LIDAIQDLPAY 132
DB 121 IYDAIDNLNPAY 132
RESULT 11
Q9TOR8 PRELIMINARY; PRT; 132 AA.
ID Q9TOR8
AC Q9TOR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alilevivirus.
OX NCBI_Taxid=75725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta".
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis".
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059243; AAC14703.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IBA.
DR GO; GO:0005198; F:structural molecule activity; IBA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
SQ SEQUENCE 132 AA; 14143 MW; 6727093757F22EA CRC64;
Query Match 74.3%; Score 493.5; DB 2; Length 132;
Best Local Similarity 74.2%; Pred. No. 3.8e-40;
Matches 98; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
QY 1 ARLEVTTLGNIGRDGQTLVLPNGVNPPTNGVSLSQAGVAPLAEKRVTVSOPSRRNK 60
DB 2 AKLNQVTLKIGKNGQTLTLTPRGVNPPTNGVSLSEAGVAPLAEKRVTVSVAQPSRRNK 61
QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDBERAFVTELAALLASPL 120
DB 62 NFKVQKIQNPACTCTRD-ACDPSVTRSGSRDVTLSFTSYSTDBERALLITELALLADPL 120
QY 121 LIDAIQDLPAY 132
DB 121 IYDAIDNLNPAY 132
RESULT 12
O64310 PRELIMINARY; PRT; 330 AA.
ID O64310
AC O64310;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC Allollevirus.
 OX NCBI_TaxID=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -.
 DR HSSP; P03615; IOBE.
 DR GO; GO:0019028; C.viral capsid; IEA.
 DR GO; GO:0005198; F.structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR InterPro; PS00030; RRM_RNP_1; UNKNOWN 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 330 AA; 36175 MW; 96155F408334410 CRC64;
 Query Match 74.3%; Score 493.5; DB 2; Length 330;
 Best Local Similarity 74.2%; Pred. No. 1,1e-39;
 Matches 98; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
 QY 1 ARLETTLIGIGDQKQTLVLRGVNPTNGVSLSGAGVPALEKRVTVSVQSPSRNK 60
 DB 2 AKNKVTLTGIGAGNQTTLTRGVNPTNGVSLSGAGVPALEKRVTVSVQSPSRNK 61
 QY 61 NYKQVQKIQNPACTANGSCDPSVTRQKADVTFSTQSTDERAFVRLTAALLASPL 120
 DB 62 NYKQVQKIQNPACTANGSCDPSVTRQKADVTFSTQSTDERAFVRLTAALLASPL 120
 QY 121 LIDAIQDLPAY 132
 DB 121 IVDAILDLPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR STANDARD; PRT; 131 AA.
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OX NCBI_TaxID=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhaese P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1.";
 RL Eur. J. Biochem. 94:375-386(1979).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KW Coat protein; Direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7E639E1E50FC612 CRC64;

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0024;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTLVLRGVNPT-----NGVASLSQAGVPALEKRVTVSVQSPSRNKKNKQV 66
 DB 4 QNLVLDRKATPDHPTFPVDIRDNVGEVSESGVIGSRFTSLRKTSNGR--YKSTL 61
 QY 67 KIQNPT--ACTANGSCDPSVTRQKADVTFSTQSTDEER-AFVRTELAALLASPLLI- 122
 DB 62 KLVVPVQGTGTVGITYPVPVVRISYTVDPDYARSTTKERNNFVGMADALGADMLVH 121
 QY 123 DAIDQDLPAY 132
 DB 122 DRIVNLQGVY 131
 RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2 PRELIMINARY; PRT; 473 AA.
 AC Q8VDC2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Trmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kiss H., Darai E., Kiss C., Kost-Alimova M., Klein G., Dumaneki J.P.,
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3.";
 RL Mamm. Genome 13:646-655(2002).
 DR EMBL; AJ428064; CAD20986.1; -.
 DR MGI; MGI:2446841; Trmem7.
 DR GO; GO:0016021; C.integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0EE69F2A4D CRC64;
 Query Match 14.5%; Score 96.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 0.88;
 Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;
 QY 5 TVTLGNIGRDGKQTLV-----LNRGVNPTNG--VASLSQAGVPALEKRVTVSVQSPSRNK 46
 DB 195 TATCSNISSSQSPSKVQMPQASKANQASNPTRKNDPKVCTSKPAPPLSPSTLSKAREP 254
 QY 47 RLVTVSVQSPSRNKKNKQV-----KIQNPT-----ACTANGSCDPSVTRQK 87
 DB 255 KLVTVCSNISSSSSSKVQMPQASKANQASNPTRKNDPKVCTSKPAPPLSPSTLSKAREP 314
 QY 88 -----KYADVTFSTQSTDERAFVRLTAALLASPLLI 122
 DB 315 SPAPAPTCVIGMPSTPTIDSGRAADVAKENRSTKTPK-----ALLSPLVY 361
 RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE STANDARD; PRT; 530 AA.
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligeriolysin precursor (Thiol-activated cytolysin).
 GN Name=Iso;
 OS Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

```

OX NCBI_TaxID=1640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLCC;
RX MEDLINE=92182018; PubMed=1543752;
RA Haas A.; Dumbeky M.; Kreft J.;
RT "Listeriolysin genes: complete sequence of ilo from Listeria ivanovi
and of iso from Listeria seeligeri.";
RL Biochim. Biophys. Acta 1130:81-84(1992).
CC -! FUNCTION: Sulphydryl-activated toxin. Is able to lyse cholesterol
containing membranes. Can be reversibly inactivated by oxidation.
CC Cholesterol is the receptor for the binding of these toxins to
CC eukaryotic cell membranes.
CC -! SIMILARITY: Belongs to the thiol-activated cytolysin family.
CC -----
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CC -----
DR EMBL; X60462; CAA42996.1; -.
DR PIR; S22340; S22340.
DR HSSP; P19995; 1PFO.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PRO1400; TACTOLYSIN.
DR PRODOM; PD007062; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOLECYTOLYSINS; 1.
KW Cytolysis; Hemolysis; Lipid-binding; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 530 Seeligeriolysin.
FT SITE 485 485 Binding to cholesterol (By similarity).
SQ SEQUENCE 530 AA; 59181 MW; 416F7A4DD2029866 CRC64;

Query Match 13.2%; Score 87.5; DB 1; Length 530;
Best Local Similarity 24.3%; Pred. No. 7.6;
Matches 33; Conservative 23; Mismatches 37; Indels 43; Gaps 7;

QY 13 RDGKQTLV--NPRGVNPT-----NGVASLSQAGA-----VPALEKRV 48
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 94 KDGSEYIVVEKKKKGINNADISVINAIISLTYPGALVKANRELVENQPNVLVVKRDSL 153
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 49 TVSVSQSPSNRRKKYKQVKNQNTACTANGSCDPSVTR--QKY-----ADVTFSFTQ 98
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 154 TUSVDLPGMTKKDKNKLFRK--NPTKSNVNNAVNTLVERWMDKYSKAYPINAKIDYS--- 208
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 99 YSTDERAFVFTETLAA 114
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB 209 ----DEMAYSESQLIA 220

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Search completed: January 4, 2005, 09:16:16
 Job time : 37.2676 secs

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CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,7e-63;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTITGKIGKQKQKOTLVNPRGVNPTNGVASISQAGVPALEKRYTVSVSOPSRNRK 60
 |||||
 Db 1 AKLEVTITGKIGKQKQKOTLVNPRGVNPTNGVASISQAGVPALEKRYTVSVSOPSRNRK 60
 |||||
 Qy 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTSTFYSTDEBERAFVTEIAALLASPL 120
 |||||
 Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTSTFYSTDEBERAFVTEIAALLASPL 120
 |||||
 Qy 121 LIDAIDQNPAY 132
 |||||
 Db 121 LIDAIDQNPAY 132
 |||||

RESULT 2

ID ABG80629 standard; protein; 132 AA.

XX ABG80629;
 AC
 XX 29-NOV-2002 (first entry)

DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-243.

KM Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IGF-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.
 OS Synthetic.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-1B000168.

XX 19-JAN-2001; 2001US-0262379P.
 XX 04-MAY-2001; 2001US-0288549P.
 XX 05-OCT-2001; 2001US-0326598P.
 XX 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUBO/) LUBOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.

XX Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;
 PI Renner W, Bachmann M, Tisost A, Seibel P, Plosssek C;
 XX WPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

PS Example 18; Page 144; 418pp; English.

CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organism comprising at least one first attachment
 CC site, where the organism is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGF-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy, immunoblastic lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,7e-63;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTITGKIGKQKQKOTLVNPRGVNPTNGVASISQAGVPALEKRYTVSVSOPSRNRK 60
 |||||
 Db 1 AKLEVTITGKIGKQKQKOTLVNPRGVNPTNGVASISQAGVPALEKRYTVSVSOPSRNRK 60
 |||||
 Qy 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTSTFYSTDEBERAFVTEIAALLASPL 120
 |||||
 Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTSTFYSTDEBERAFVTEIAALLASPL 120
 |||||
 Qy 121 LIDAIDQNPAY 132
 |||||
 Db 121 LIDAIDQNPAY 132
 |||||

RESULT 3
 ABR56453
 ID ABR56453 standard; protein; 132 AA.

XX ABR56453;
XX
XX 28-JUL-2003 (first entry)
XX
XX Bacteriophage Q-beta coat protein mutant SEQ ID NO:24.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
XX cytosolic; virucide; antibacterial; antiparasitic; fungicide;
XX antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
XX antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
XX antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
XX anti-viral protection; tumor; allergy; drug addiction; Crohn's disease;
XX graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
XX Alzheimer's disease; osteoporosis; rheumatoid arthritis;
XX inflammatory autoimmune disease.
XX
XX Bacteriophage Qbeta.
XX Synthetic.
XX
XX WO2003024480-A2.
XX
XX 27-MAR-2003.
XX
XX 16-SEP-2002; 2002MO-IB004252.
XX
XX 14-SEP-2001; 2001US-0318967P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann MF, Storni T, Lechner F;
XX
XX WPI; 2003-363095/34.
XX
XX
XX A composition, useful for enhancing an immune response against an antigen
XX or a virus-like particle, enhancing anti-viral protection in an animal,
XX or immunizing or treating tumors or infectious diseases, e.g. viral
XX infections.
XX
XX
XX Disclosure; Page 180-181; 243p; English.
XX
XX
XX The present invention describes a composition (C) for enhancing an immune
XX response against an antigen or a virus-like particle in an animal. (C)
XX comprises a virus-like particle (VLP) bound to at least one antigen, or a
XX VLP capable of being recognised by the immune system of the animal. Also
XX described: (1) enhancing an immune response against an antigen or a VLP
XX in an animal comprising introducing (C) into the animal; (2) vaccines
XX comprising (C) together with a pharmaceutical diluent, carrier or
XX excipient; (3) immunising or treating an animal comprising administering
XX the vaccine to the animal, or priming or boosting a T cell response in
XX the animal by administering the vaccine; and (4) enhancing anti-viral
XX protection in an animal comprising introducing (C) into the animal. (C)
XX has cytosolic, virucide, antibacterial, antiparasitic, fungicide,
XX antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
XX antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
XX antirheumatic and antiarthritic activities. (C) or the vaccines can be
XX used for enhancing an immune response against an antigen or a VLP in an
XX animal, enhancing anti-viral protection in an animal, or immunising or
XX treating tumors and infectious diseases such as viral, bacterial,
XX parasitic or fungal infections. The vaccine compositions are also useful
XX for preventing or treating allergies, drug addiction, graft-versus-host
XX disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
XX Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
XX autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
XX
XX Query Match 100.0%; Score 663; DB 6; Length 132;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-69;
XX Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX

Db		1 AKLEIVTLTGKIGDKQITLVNPRGVNPINGVASLSQAQAVPALERGVTVSVSQPSRNRK 60
Oy	61	NKKVQVKIQNPFCTANGSCDPSVTROKKYADVTFSFTQYSTDERAFVETELAAALASPL 120
Dd	61	NKKVQVKIQNPFCTANGSCDPSVTROKKYADVTFSTQYSTDERAFVETELAAALASPL 120
Oy	121	LIDAIDQLNPAY 132
Dd	121	LIDAIDQLNPAY 132
		RESULT 4
	ABU09690	ABU09690 standard; protein; 132 AA.
XX		
AC	ABU09690;	
XX		
DT	03-JUL-2003	(first entry)
XX		
DE	Bacteriophage Qbeta mutant coat protein #2.	
XX		
KW	Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;	
KM	cardiac; nephroretic; ophthalmological; immunostimulant; vaccine;	
KM	angiotensin peptide moiety carrier conjugate; angiotensin peptide;	
KM	renin-activated angiotensin system; hypertension; stroke; infection;	
KW	congestive heart failure; kidney failure; retinal haemorrhage; mutant;	
muetcn.		
XX		
OS	Bacteriophage Qbeta.	
XX		
PN	WO2003031466-A2.	
PD		
XX	17-APR-2003.	
PF	07-OCT-2002; 2002MO-EP011219.	
XX		
PR	05-OCT-2001; 2001US-0326998P.	
PR	07-NOV-2001; 2001US-0331045P.	
PR	18-JAN-2002; 2002US-00050902.	
PR	21-JAN-2002; 2002MO-IB000166.	
PR	19-JUL-2002; 2002US-0396637P.	
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
PI	Bachmann M;	
XX		
DR	WPI; 2003-430264/40.	
PT	New angiotensin peptide moiety carrier conjugate comprising a carrier and	
PT	an angiotensin peptide moiety, useful for treating or preventing a	
PT	disorder associated with renin-activated angiotensin, e.g. hypertension	
PT	or infection.	
PS	Claim 20; Page 94; 97pp; English.	
XX		
CC	The invention describes an angiotensin peptide moiety carrier conjugate	
CC	comprising: (a) a carrier with at least one first attachment site; and	
CC	(b) at least one angiotensin peptide moiety with at least one second	
CC	attachment site. The angiotensin peptide conjugate and compositions	
CC	comprising them are useful for immunising an animal against an	
CC	angiotensin peptide, and for treating or preventing a physical disorder	
CC	associated with renin-activated angiotensin system such as hypertension,	
CC	stroke, infarction, congestive heart failure, kidney failure, and retinal	
CC	haemorrhage. The conjugate is also useful for inducing immune responses,	
CC	including producing antibodies. This is the amino acid sequence of a	
CC	mutant bacteriophage Qbeta coat protein used in the preparation of the	
CC	vaccine conjugates of the invention	
XX		
SQ	Sequence 132 AA:	
	Query Match 100.0%; Score 663; DB 6; Length 132;	
	Best Local Similarity 100.0%; Pred. No. 2,76-69;	

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGKDGKOTLVINPRGVNPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 AKLEVTTLGKIGKDGKOTLVINPRGVNPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

QY 61 NYKVQVXIONPTACTANGSCDPSVTRQKXADVTFSTQYSTDERRAFVRELAALLASPL 120
 DB 61 NYKVQVXIONPTACTANGSCDPSVTRQKXADVTFSTQYSTDERRAFVRELAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 5
 ABR44556
 ID ABR44556 standard; protein; 132 AA.
 AC ABR44556;
 DT 25-JUL-2003 (first entry)

DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:24.

KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; anti-allergic; virocidic; antibacterial;
 KW immune response; immunisation; allergy; tumor; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

OS Bacteriophage Qbeta.
 OS Synthetic.
 PN WO2003024481-A2.
 PD 27-MAR-2003.
 PF 16-SEP-2002; 2002WO-IB004132.
 PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER P.
 PA (TISSOT A.
 PA (SCHWAB) SCHWARZ K.
 PA (MEITZ) MEIERINK E.
 PA (LIPPO) LIPOWSKI G.
 PA (PUMP) PUMPENS P.
 PA (CIEL) CIELENS I.
 PA (REINH) REINHOF A R.

PI Maurer P, Tisot A, Schwarz K, Meierink E, Lipowski G;
 PI Pumpens P, Cielens I, Reinhold R, Bachmann M, Storni T;
 PI WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.

XX Disclosure; Page 260; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, anti-allergic, virocidic and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention

XX Sequence 132 AA;
 SQ

Query Match 100.0%; Score 663; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGKDGKOTLVINPRGVNPTNGVASLSQAGAVPALERKVTVSQPSNRK 60
 DB 1 AKLEVTTLGKIGKDGKOTLVINPRGVNPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

QY 61 NYKVQVXIONPTACTANGSCDPSVTRQKXADVTFSTQYSTDERRAFVRELAALLASPL 120
 DB 61 NYKVQVXIONPTACTANGSCDPSVTRQKXADVTFSTQYSTDERRAFVRELAALLASPL 120

QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 6
 ADD24131
 ID ADD24131 standard; protein; 132 AA.
 AC ADD24131;
 DT 15-JAN-2004 (first entry)

DE Bacteriophage Qbeta coat protein mutant Qbeta-243.

KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; anti-inflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob disease; coat protein; mutant; mutagen.

OS Synthetic.
 OS Bacteriophage Qbeta.
 PN WO2003059386-A2.
 PD 24-JUL-2003.

XX 17-JAN-2003; 2003WO-EP000460.
 XX 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER P.
 PA (FELICCIOLI E.
 PA (RENNER W.A.
 PI Bachmann M, Maurer P, Feliccioli E, Renner W.A;
 PI WPI; 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.

PT Hodgkin's lymphoma.
 XX
 PS Disclosure; SEQ ID NO 24; 245pp; English.
 XX
 CC The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC antigen with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medicaments, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.
 XX
 SQ Sequence 132 AA;
 Query Match 100.0%; Score 663; DB 7; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 DB 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
 DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 RESULT 9
 ADJ36314
 ID ADJ36314 standard; protein; 132 AA.
 XX
 AC ADJ36314;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Bacteriophage Qbeta coat protein virus-like particle mutant K13R.
 XX
 KW anti-allergic; cytostatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage Qbeta;
 KW coat protein; VLP; adjuvant; mutant; mutain.
 XX
 OS Bacteriophage Qbeta.
 XX
 PN WO2004000351-A1.
 XX
 PD 31-DEC-2003.
 XX
 PF 20-JUN-2003; 2003WO-EP006541.
 XX
 PR 20-JUN-2002; 2002US-0389898P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann MF, Renner WA;
 XX
 DR WPI; 2004-108361/11.
 XX
 PT New compositions comprising a virus-like particle (VLP), an
 PT immunostimulatory substance bound to the VLP, and an antigen mixed with
 PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
 XX
 PS Disclosure; SEQ ID NO 15; 252pp; English.
 XX
 CC The invention describes a composition for enhancing an immune response in
 CC an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
 CC coat protein mutant, a virus like particle (VLP) that can be used in the
 CC adjuvant of the invention.
 XX
 SQ Sequence 132 AA;
 Query Match 100.0%; Score 663; DB 8; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.7e-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 DB 1 AKLEVTYLGKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSQPSRRNK 60
 QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
 DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 RESULT 10
 ADJ67160
 ID ADJ67160 standard; protein; 132 AA.
 XX
 AC ADJ67160;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Phage Qbeta coat protein mutant Qbeta 243 for antigen display array.
 XX
 KW anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
 KW antigenic array.
 XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 PN WO2004009124-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007849.
 XX
 PR 19-JUL-2002; 2002US-0396638P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann MF, Fulurija A;
 XX
 DR WPI; 2004-132866/13.
 XX
 PT New composition comprising a core particle having a first attachment site
 PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
 PT peptide having a second attachment site, useful for treating obesity.
 XX
 PS Disclosure; SEQ ID NO 18; 175pp; English.
 XX
 CC The invention relates to a new composition comprising: (i) a core
 CC particle with at least one first attachment site; and (ii) at least one
 CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
CC peptide, and where the second attachment site being consisting of an
CC attachment site not naturally occurring with the antigen or antigenic
CC determinant and an attachment site naturally occurring with the antigen
CC or antigenic determinant, where the second attachment site is capable of
CC association to the first attachment site, and where the ghrelin or a
CC ghrelin peptide and the core particle interact through the association to
CC form an ordered and repetitive antigen array. The composition is useful
CC for treating obesity. The repetitive array may form part of a phage or
CC bacterial display array. This peptide corresponds to a Bacteriophage
CC Qbeta coat protein mutant which can used as part of the repetitive or
CC antigenic array.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.7e-69; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
DB 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFRTIELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFRTIELAALLASPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132

RESULT 11

ADK52194
ID ADK52194 standard; protein; 132 AA.

XX ADK52194;

XX 20-MAY-2004 (first entry)

XX Bacteriophage Qbeta coat protein mutant N10K.

XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
XX core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
XX coat protein; CP; mutant; mutein.

XX Bacteriophage Qbeta.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 10 /note= "Wild type Asn substituted by Lys"

XX WO2004016282-A1.

XX 26-FEB-2004.

XX 18-JUL-2003; 2003WO-EP007864.

XX 19-JUL-2002; 2002US-0396639P.

XX 15-MAY-2003; 2003US-0470432P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX (NOVS) NOVARTIS PHARMA AG.

XX Bachmann M, Tisot A, Ottmann R, Lucend R, Staufendiel M,

XX Frey P;

XX WPI, 2004-203731/19.

XX Composition comprising a core particle with at least one attachment site,
XX and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
XX such as Alzheimer's disease.

XX Example 1; SEQ ID NO 18; 184bp; English.

PS The invention describes a novel composition comprising a virus-like core
XX particle with at least one attachment site, and an antigenic amyloid beta
XX 1-6 peptide. The new composition comprises: a core particle with at least
CC one first attachment site; and at least one antigen or antigenic
CC determinant with at least one second attachment site, where the antigen
CC or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
CC second attachment site comprises: an attachment site not naturally
CC occurring with the antigen or antigenic determinant; or an attachment
CC site naturally occurring with the antigen or antigenic determinant. The
CC second attachment site is capable of association to the first attachment
CC site and the beta 1-6 peptide and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC composition is useful for the manufacture of a medicament for treating
CC Alzheimer's disease and related diseases. This is the amino acid sequence
CC of an RNA bacteriophage Qbeta coat protein mutant that can be used in the
CC preparation of the compositions and vaccines of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.7e-69; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
DB 1 AKLEVTTLGKIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFRTIELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFRTIELAALLASPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132

RESULT 12

ABG94316
ID ABG94316 standard; protein; 132 AA.

XX ABG94316;

XX 29-AUG-2003 (revised)

XX 10-DEC-2002 (first entry)

XX P0B240 protein.

XX Human; mouse; rat; antimicrobial; antifungal; immunomodulatory;
XX cytoskeletal; antiviral; antidiabetic; hypoglycaemic; antigen array;
XX vaccine; infectious disease.

XX unidentified bacteriophage.

XX WO200256905-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-1B000166.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326989P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Renner WA, Bachmann M, Tisot A, Maurer P, Lechner F, Sebbel P,

XX Ploesek C;

XX WPI, 2002-627351/67.

XX Molecular antigen array used in the production of vaccines for infectious diseases.

PS Claim 18; Page 144; 441pp; English.

CC This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffold comprising a core particle selected from a core particle of a non-natural origin and a core particle of natural origin and an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (Abeta1-42) or its fragment and where the second attachment site is selected from an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Qbeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention. (Updated on 29 AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 98.8%; Score 655; DB 5; Length 132;

Best Local Similarity 98.5%; Pred. No. 2.4e-68; Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTYTGKIGDKQTLVLPNGVPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 DB 1 AKLEVTYTGKIGDKQTLVLPNGVPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 QY 61 NKVQVKIQNPACTANGSCDPSVTRKXADYTFSTQYSTDEBAFVTELAALLASPL 120
 DB 61 NKVQVKIQNPACTANGSCDPSVTRKXADYTFSTQYSTDEBAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 13

ABG94320 ABG94320 standard; protein; 132 AA.

XX ABG94320;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

DE PQB251 protein.

XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory; cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;

XX vaccine; infectious disease.

OS unidentified bacteriophage.

XX WO200256905-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002MO-IB000166.

XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Renner WA, Bachmann M, Tisect A, Maurer P, Lechner F, Seibel P;
 PI Ploesser C;

DR WPI; 2002-627351/67.

PT Molecular antigen array used in the production of vaccines for infectious diseases.

PS Claim 18; Page 426; 441pp; English.

CC This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffold comprising a core particle selected from a core particle of a non-natural origin and a core particle of natural origin and an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (Abeta1-42) or its fragment and where the second attachment site is selected from an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Qbeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention. (Updated on 29 AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 98.8%; Score 655; DB 5; Length 132;

Best Local Similarity 98.5%; Pred. No. 2.4e-68; Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLEVTYTGKIGDKQTLVLPNGVPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 DB 1 AKLEVTYTGKIGDKQTLVLPNGVPTNGVASLSQAGAVPALERKRVTSVSQPSRRNK 60
 QY 61 NKVQVKIQNPACTANGSCDPSVTRKXADYTFSTQYSTDEBAFVTELAALLASPL 120
 DB 61 NKVQVKIQNPACTANGSCDPSVTRKXADYTFSTQYSTDEBAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 14

ABG80632 ABG80632 standard; protein; 132 AA.

XX ABG80632;

XX 29-NOV-2002 (first entry)

XX Bacteriophage Q-beta A1 coat protein mutant Qbeta-259.

KW Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; Igs-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 XX Bacteriophage Qbeta.
 OS Synthetic.
 XX WO200256907-A2.
 XX 25-JUL-2002.
 XX 21-JAN-2002; 2002WO-IB000168.
 XX 19-JAN-2001; 2001US-0262379P.
 XX 04-MAY-2001; 2001US-0288549P.
 XX 05-OCT-2001; 2001US-0326998P.
 XX 07-NOV-2001; 2001US-0331045P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX (NOVS) NOVARTIS PHARMA AG.
 XX (MAUR/) MAURER P.
 XX (LECH/) LECHNER F.
 XX (ORTM/) ORTMANN R.
 XX (LUBO/) LUBOEND R.
 XX (STAU/) STAUFENBIEL M.
 XX (FREY/) FREY P.
 XX Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;
 XX Renner W, Bachmann M, Tissot A, Sebbel P, Ploessek C;
 XX WPI; 2002-636514/68.
 XX Molecular antigen array used in the production of vaccines for infectious
 XX diseases.
 XX Example 18, Page 146, 418pp; English.
 XX The invention relates to a composition comprising: (a) a non-natural
 XX molecular scaffold comprising: (i) a core particle selected from: (1) a
 XX core particle of a non-natural origin; and (2) a core particle of natural
 XX origin; and (ii) an organism comprising at least one first attachment
 XX site, where the organism is connected to the core particle by at least
 XX one covalent bond; (b) an antigen or antigenic determinant with at least
 XX one second attachment site, where the antigen or antigenic determinant is
 XX amyloid beta peptide (Abeta 1-42) or its fragment; and where the second
 XX attachment site is selected from: (i) an attachment site not naturally
 XX occurring with the antigen or antigenic determinant; and (ii) an
 XX attachment site naturally occurring with the antigen or antigenic
 XX determinant, where the second attachment site is capable of association
 XX through at least one non-peptide bond to the first attachment site; and
 XX where the antigen or antigenic determinant and the scaffold interact
 XX through the association to form an ordered and repetitive antigen array.
 XX Also included is a process for producing a non-naturally occurring
 XX ordered and repetitive antigen array. The composition is used in
 XX immunisation and as a vaccine for diseases such as influenza, graft
 XX versus host disease, Igs-mediated allergic reactions, anaphylaxis, adult
 XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 XX gravis, immunoproliferative disease lymphadenopathy,
 XX angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 XX osteoporosis and infectious diseases. The antigens are modified to possess
 XX a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 XX or C-terminal linker peptide which serves as the attachment point to a

CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 XX
 SQ Sequence 132 AA;
 Query Match 98.8%; Score 655; DB 5; Length 132;
 Best Local Similarity 98.5%; Pred. No. 2.4e-68;
 Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AKLEVTGKIGKQKQKLTLPNPGVPTNGVASISQAGVPALEKRTVSVSOPSRRK 60
 DB 1 AKLEVTGKIGKQKQKLTLPNPGVPTNGVASISQAGVPALEKRTVSVSOPSRRK 60
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERRAFVTEIAALLASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERRAFVTEIAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 DB 121 LIDAIDQLNPAY 132
 RESULT 15
 ABG80628
 ID ABG80628 standard; protein; 132 AA.
 XX
 AC ABG80628;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-240.
 XX
 KW Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; Igs-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 XX Bacteriophage Qbeta.
 OS Synthetic.
 XX WO200256907-A2.
 XX 25-JUL-2002.
 XX 21-JAN-2002; 2002WO-IB000168.
 XX 19-JAN-2001; 2001US-0262379P.
 XX 04-MAY-2001; 2001US-0288549P.
 XX 05-OCT-2001; 2001US-0326998P.
 XX 07-NOV-2001; 2001US-0331045P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX (NOVS) NOVARTIS PHARMA AG.
 XX (MAUR/) MAURER P.
 XX (LECH/) LECHNER F.
 XX (ORTM/) ORTMANN R.
 XX (LUBO/) LUBOEND R.
 XX (STAU/) STAUFENBIEL M.
 XX (FREY/) FREY P.
 XX Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;
 XX Renner W, Bachmann M, Tissot A, Sebbel P, Ploessek C;
 XX WPI; 2002-636514/68.
 XX

PT Molecular antigen array used in the production of vaccines for infectious PT diseases.

PS Example 18; Page 144; 418pp; English.

The invention relates to a composition comprising: (a) a non-natural molecular scaffold comprising: (i) a core particle selected from: (1) a core particle of a non-natural origin; and (2) a core particle of natural origin; and (ii) an organismer comprising at least one first attachment site, where the organismer is connected to the core particle by at least one covalent bond; (b) an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (A β 1-42) or its fragment, and where the second attachment site is selected from: (i) an attachment site not naturally occurring with the antigen or antigenic determinant; and (ii) an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site; where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. Also included is a process for producing a non-naturally occurring ordered and repetitive antigen array. The composition is used in immunisation and as a vaccine for diseases such as influenza, graft versus host disease, IgE-mediated allergic reactions, anaplasia, adult respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease, systemic lupus erythematosus, inflammatory immune diseases, myasthenia gravis, immunoproliferative disease lymphadenopathy, angioimmunoproliferative lymphadenopathy, immunolactive lymphadenopathy, rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis and infectious diseases. The antigens are modified to possess a cleavage site (elastase or factor Xa) and a attachment point to a C-terminal linker peptide which serves as the attachment point to a virus like particle or bacterial protein (the scaffold protein). The present sequence is bacterial protein or peptide which is coupled to the modified antigen to form the molecular antigen array

SQ Sequence 132 AA;

Query Match	98.8%	Score 655;	DB 5;	Length 132;
Best Local Similarity	98.5%	Pred: No.2.4e-68;		
Matches 130; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 AKLEETVLGKIGDGKQKOTLVLPNGVNPPTNGVSLSSAGAVPMLERKVTIVSVQPSNNRK 60

Db 1 AKLEETVLGNIGRGRQOTLVLPNGVNPPTNGVSLSSAGAVPMLERKVTIVSVQPSNNRK 60

QY 61 NPKYQVNIQNPCTACTANGSCDSPSTRQKADVTFPSFYQSTDEERAFVRELAAIILASPL 120

Db 61 NPKYQVNIQNPCTACTANGSCDSPSTRQKADVTFPSFYQSTDEERAFVRELAAIILASPL 120

QY 121 LIDAIIDLNPAY 132

Db 121 LIDAIIDLNPAY 132

Search completed: January 4, 2005, 09:11:01
Job time : 40.6824 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 09:05:21 ; Search time 10.3622 Seconds
(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-7

Perfect score: 663
Sequence: 1 AKETVTLGKIGKDGKQTLV.....ALLASPLIDALDQLNPAY 132

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 segs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiletest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.5	12.7	626	4	US-09-485-717-2
2	84.5	12.7	626	4	US-09-948-722-2
3	72.5	10.9	916	4	US-09-252-991A-23637
4	72	10.9	409	4	US-09-328-352-4249
5	70.5	10.6	502	4	US-09-270-767-44620
6	70.5	10.6	2042	4	US-09-077-098A-6
7	70	10.6	233	3	US-08-725-459B-45
8	70	10.6	341	3	US-08-725-459B-44
9	70	10.6	434	3	US-08-725-459B-42
10	69.5	10.5	129	1	US-08-090-148-1
11	69	10.4	273	3	US-08-235-836C-11
12	69	10.4	273	3	US-08-235-836C-89
13	68.5	10.3	383	3	US-09-045-186-2
14	68.5	10.3	384	1	US-08-232-144-4
15	68.5	10.3	384	2	US-08-555-268A-15
16	68.5	10.3	384	3	US-09-200-673-15
17	68.5	10.3	384	4	US-10-013-846-4
18	68.5	10.3	384	4	US-09-708-392-9
19	68.5	10.3	384	5	PCT-US93-05039-3
20	68.5	10.3	411	3	US-08-817-869-3
21	68.5	10.3	411	5	PCT-US95-14377-3
22	68.5	10.3	733	4	US-09-248-796A-16565
23	68	10.3	316	4	US-09-270-767-43925
24	68	10.3	316	4	US-09-270-767-59331
25	67.5	10.2	424	3	US-09-173-581-7
26	67.5	10.2	424	3	US-09-420-915-7
27	67.5	10.2	1328	3	US-08-781-891-76

28	67.5	10.2	1328	4	US-09-618-166-76	Sequence 76, Appl
29	66.5	10.0	141	4	US-09-248-796A-16789	Sequence 16789, A
30	66.5	10.0	279	3	US-08-397-411-13	Sequence 13, Appl
31	66.5	10.0	518	4	US-09-248-796A-20249	Sequence 20249, A
32	66.5	10.0	818	4	US-09-252-991A-16691	Sequence 16691, A
33	66	10.0	345	3	US-08-856-253-7	Sequence 7, Appl
34	66	10.0	737	4	US-09-071-035-460	Sequence 460, App
35	66	10.0	933	3	US-08-421-868-2	Sequence 2, Appl
36	66	10.0	936	4	US-09-956-171B-5249	Sequence 5249, Ap
37	66	10.0	936	4	US-08-781-986A-5249	Sequence 5249, Ap
38	66	10.0	936	4	US-08-720-484A-5	Sequence 5, Appl
39	66	10.0	1036	2	US-08-953-823A-5	Sequence 5, Appl
40	66	10.0	1036	4	US-09-398-239-5	Sequence 5, Appl
41	66	10.0	1036	4	US-09-560-876A-5	Sequence 5, Appl
42	66	10.0	1065	4	US-09-560-876A-6	Sequence 6, Appl
43	66	10.0	1281	2	US-08-843-530B-6	Sequence 6, Appl
44	66	10.0	1281	4	US-09-636-728-5	Sequence 5, Appl
45	66	10.0	1281	4	US-09-636-728-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-09-485-717-2
; Sequence 2, Application US/09485717
; Patent No. 6673353
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 16862PUS
; CURRENT APPLICATION NUMBER: US/09/485,717
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: EP 97114614.7
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/EP98-05109
; PRIOR FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2
Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best Local Similarity 22.7%; Pred. No. 0.14;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KDGGQTLVL-----NPRGVNPTNGVASLSQAG-----VPALEKRV 48
DB 138 KDGGYIVVEKKKINSQNNADIQVNAISLTFYFGALVANSSELVENQDVLVKKDSLT 197
QY 49 TVSSQSSRRKKKKVQVQKQNPACTANGSCDSVTR-----QKADYTFSTQVSTD 102
DB 198 TLTSLDGLQMTQNDKKIVK--NATKSNVNNNAVTLVERMKVKQAQAVPNVS---AKIDYD 252
QY 103 EERAFVTELLA 114
DB 253 DEMAYSESQLLA 264
RESULT 2
US-09-948-722-2
; Sequence 2, Application US/09948722
; Patent No. 6776993
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan H. E.
; APPLICANT: Hess, Jurgen
; TITLE OF INVENTION: Tuberculosis Vaccine
```

FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysomal
OTHER INFORMATION: escape domain
US-09-948-722-2

Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best Local Similarity 22.7%; Pred. No. 0.14;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGKQTLV-----NPRGVNPTNGVASLSQAGA-----VPALRKRV 48
DB 138 KGNEXYIVAEKKKKSINQNNADIQVNNALISLTPGALVKANSELVENQPDVLPVKRDSL 197
QY 49 TVSVSPSRNKNKYQVQKIONPCTANGSCDPSVTR-----OKYADVTFSTQYSTD 102
DB 198 TISIDLPKNTNDNKTIVK--NATKSNVNNVAVTTLVERNNKTKAQIVPVS---AKIDVD 252
QY 103 EERAFVTEIAA 114
DB 253 DEMAYSESQLIA 264

RESULT 3
US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637

Query Match 10.9%; Score 72.5; DB 4; Length 916;
Best Local Similarity 22.9%; Pred. No. 8.6; Mismatches 53; Indels 21; Gaps 4;
Matches 27; Conservative 17

QY 9 GKIGKDG-----KQTLVNPGRVPTNGVASLSQAGAVPALRKRVTVSVS-----QP 55
DB 789 GLGGBEALRLRAIYVQARRIDPFGGLAALPVGGLPALBQEDPAFGSLDQRWQA 848
QY 56 SRNKNKYQVQKIONPCTANGSCDPSVTRQKADVTFSSTQYSTDEERAFVTT 110
DB 849 EERGAIFYRAQBSAHEHPCRSIEANADCPISADAGK-----PWTIFSDATRWALRT 901

RESULT 4
US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562358
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match 10.9%; Score 72; DB 4; Length 409;
Best Local Similarity 25.0%; Pred. No. 2.8;
Matches 26; Conservative 18; Mismatches 44; Indels 16; Gaps 4;

QY 26 VNPTNGVASLSQAGAVPALRKRVTVSVSPSRNKNKYQVQKIONPCTANGSCDPSV 84
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QY 85 TRQKADVTFSSTQYSTDEERAFVTEIAALLASPLIDAIDQL 128
DB 189 TAKPYSEITP-----EENVESYKTIHMLKASKQIIDLDPOL 225

RESULT 5
US-09-270-767-44620
Sequence 44620, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44620
LENGTH: 502
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44620

Query Match 10.6%; Score 70.5; DB 4; Length 502;
Best Local Similarity 24.2%; Pred. No. 6;
Matches 29; Conservative 20; Mismatches 52; Indels 19; Gaps 4;

QY 18 TLVNPGRVPTNGVASLSQAGAVPALRKRVTVSVSP-----SRNKNKYQVQKION 70
DB 258 TLAVN---ISPSPPPTQPIPEVEQVENSVTIVASPEVPVAXARNRKRQTRSTICK 314
QY 71 PRACTANGSCDPSVTRQKADVTFSSTQ-----YSTDEERAFVTT---ELAAALASP 121
DB 315 AXVVKYFSCSTSATRHSSTRCISVYSOSLGPSPILGXADKDFVTLKPLATFSSPWL 374

RESULT 6
US-09-077-098A-6
Sequence 6, Application US/09077098A
Patent No. 6544519
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
SAKAGUCHI, Masaaki
MATSUO, Kazuo
HAMADA, Fukuaburo

TKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,098A
FILING DATE: 19-May-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: KORNBAU, Anne M.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TOKUNAGA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-077-098A-6

Query Match 10.6%; Score 70.5; DB 4; Length 2042;
Best Local Similarity 27.2%; Pred. No. 54;
Matches 28; Conservative 13; Mismatches 53; Indels 9; Gaps 4;

Qy 3 LETVTLKIGKDGKQTLV-LNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNKN 61
Db 1347 LDDTLANKLNPPADDDLSLSESGKNAITGLVDV-----VKKTNSPTVEPSTDSNKKKT 1401

Qy 62 YKVOVKIONPTACTANGSCDPSVTRQYAD--VTFSTQYSTD 102
Db 1402 FTVGVDFPD-TTTEGDATDDKLTTSKSVESYVTNKLNFSTD 1443

RESULT 7
US-08-725-459B-45
Sequence 45, Application US/08725459B
Patent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
CITY: DALLAS
STATE: TX
COUNTRY: US
ZIP: 75201-6507
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..233
OTHER INFORMATION: /note="amino acids 202-434 of C."
US-08-725-459B-45

Query Match 10.6%; Score 70; DB 3; Length 233;
Best Local Similarity 32.6%; Pred. No. 21;
Matches 31; Conservative 13; Mismatches 37; Indels 14; Gaps 5;

Qy 2 KLEVTTLKIGK-----DGKQTLV-LNPRGVNPTNGVASLSQAGAV--PALEKRVTVSVS 53
Db 116 KLEMLT-SRIGKSNAGSGRGQTVWIDMAHTR---VRSKSPFNTVKDSQVMSATPSAL 170

Qy 54 OPSRNRKRYKVOVKIONPTACTANGSCDPSVTRQK 88
Db 171 QLSQARKRVKIEGKAQLRT-ITPRGGVPSYTSRSR 204

RESULT 8
US-08-725-459B-44
Sequence 44, Application US/08725459B
Patent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARWOOD, SUITE 3400
CITY: DALLAS
STATE: TX
COUNTRY: US
ZIP: 75201-6507
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..341
OTHER INFORMATION: /note="amino acids 94-434 of C."
OTHER INFORMATION: elegans"
US-08-725-459B-44

Query Match 10.6%; Score 70; DB 3; Length 341;
Best Local Similarity 32.6%; Pred. No. 3.8;
Matches 31; Conservative 13; Mismatches 37; Indels 14; Gaps 5;

QY 2 KLEVTTLGKIGK-----DGKQTLVLPNGVNPVNGVSLSQAGV--PALEKRVTVSVS 53
DB 224 KLEMLT-SRIGKNSAOSQGRQTVWIDMAHTR---VRSKSFNTVKDSQVMSATPSAL 278

QY 54 QPSRRKRYKVQVKIQNPACTANGSCDPSVTROK 88
DB 279 QLSQARKVKIKGKAQLRT-ITPRGGGVPTSTRSR 312

RESULT 9
US-08-725-459B-42
Sequence 42, Application US/08725459B
Patent No. 6084068
GENERAL INFORMATION:
APPLICANT: CONAWAY, RONALD C.
APPLICANT: CONAWAY, JOAN W.
TITLE OF INVENTION: ELONGIN A AND C FUNCTIONAL DOMAINS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIDLEY & AUSTIN
STREET: 717 N. HARMOD, SUITE 3400
CITY: DALLAS
STATE: TX
COUNTRY: US
ZIP: 75201-6507
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,459B
FILING DATE: 04-OCT-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 11146/07501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-981-3300
TELEFAX: 214-981-3400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..434
OTHER INFORMATION: /note="entire amino acid sequence
OTHER INFORMATION: of C. elegans"
US-08-725-459B-42

Query Match 10.6%; Score 70; DB 3; Length 434;

Best Local Similarity 32.6%; Pred. No. 5.5;
Matches 31; Conservative 13; Mismatches 37; Indels 14; Gaps 5;

QY 2 KLEVTTLGKIGK-----DGKQTLVLPNGVNPVNGVSLSQAGV--PALEKRVTVSVS 53
DB 317 KLEMLT-SRIGKNSAOSQGRQTVWIDMAHTR---VRSKSFNTVKDSQVMSATPSAL 371

QY 54 QPSRRKRYKVQVKIQNPACTANGSCDPSVTROK 88
DB 372 QLSQARKVKIKGKAQLRT-ITPRGGGVPTSTRSR 405

RESULT 10
US-08-090-148-1
Sequence 1, Application US/08090148
Patent No. 5534257
GENERAL INFORMATION:
APPLICANT: Mastico, Robert Allan
APPLICANT: Stockley, Peter George
APPLICANT: Talbot, Simon John
TITLE OF INVENTION: Antigen-Presenting Capsid with
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roseman & Collin
STREET: 575 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10022-2585
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44MB
COMPUTER: IBM PS2-486
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,148
FILING DATE: 08/11/93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9101550.3
FILING DATE: 01/24/91
APPLICATION NUMBER: PCT/GB92/00124
FILING DATE: 01/22/92
ATTORNEY/AGENT INFORMATION:
NAME: Nissenbaum, Israel
REGISTRATION NUMBER: 27,582
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-8636
TELEFAX: (212) 940-6404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: NOT RELEVANT
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: VIRUS
FEATURE:
NAME/KEY: Coat protein from MS2-RNA
NAME/KEY: bacteriophage
LOCATION: Location 1 through 129 below
LOCATION: represents entire MS2 coat
LOCATION: protein in the published
LOCATION: sequence.
PUBLICATION INFORMATION:
AUTHORS: Min Jou, W.; Haegeman, G.;
AUTHORS: Ysebaert, M.; Fiers, W.
TITLE: Nucleotide sequence of the
TITLE: gene coding for the
TITLE: bacteriophage MS2 coat protein
JOURNAL: Nature

VOLUME: 237
PAGES: 82-88
DATE: 1972
US-08-090-148-1

Query Match 10.5%; Score 69.5; DB 1; Length 129;

Best Local Similarity 25.0%; Pred. No. 0.94; Mismatches 43; Indels 13; Gaps 2;

Db 27 NPTNGVA-----SLSQAGVPALEKRVTVSVSOPSRNKYKVQKIONPTACTANGSC 80
24 NRVNGVAEIVSSNSQA-----KVTCSVRQSAQNRKTTIKVEKVAQTGVGVE 76

Qy 81 DSVTRQKYADYTFSEFTQYSTDEBRAVTELAAL 116
Db 77 LPVAAWRSYLMELTPIPATNSDCELIYKAMQGLL 112

RESULT 11
US-08-235-836C-11
Sequence 11, Application US/08235836C
Patent No. 6248562

GENERAL INFORMATION:

APPLICANT: Dunn, John J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:

STREET: Brookhaven National Laboratory

CITY: Upton
STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/148,191

ATTORNEY/AGENT INFORMATION:

NAME: Bogosian, Margaret C.

REGISTRATION NUMBER: 25,324

REFERENCE/DOCKET NUMBER: BNL93-28A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 282-7338

TELEFAX: (516) 282-3729

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-235-836C-11

Query Match 10.4%; Score 69; DB 3; Length 273;

Best Local Similarity 28.8%; Pred. No. 3.6; Mismatches 35; Indels 10; Gaps 3;

Db 5 TTTTGGK-IGKQKQTLVNPGRVNPNGVASLSQAGVPALEKRVTVSVSOPSRNR----- 59
184 TTTLSKEIKAKSGEVVAL-----NDTNTTQATKTKTGAMDSKSTLTISVNSKTTQVLVFT 238

Qy 60 KNYKVQVKIONPTACTANGS 79
Db 239 KQYITTVKQYDSAGTNLEGT 258

RESULT 12
US-08-235-836C-89

Sequence 89, Application US/08235836C
Patent No. 6248562

GENERAL INFORMATION:

APPLICANT: Dunn, John J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

STREET: Brookhaven National Laboratory

CITY: Upton

STATE: NY

COUNTRY: USA

ZIP: 11973

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/148,191

ATTORNEY/AGENT INFORMATION:

NAME: Bogosian, Margaret C.

REGISTRATION NUMBER: 25,324

REFERENCE/DOCKET NUMBER: BNL93-28A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 282-7338

TELEFAX: (516) 282-3729

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-235-836C-89

Query Match 10.4%; Score 69; DB 3; Length 273;

Best Local Similarity 28.8%; Pred. No. 3.6; Mismatches 35; Indels 10; Gaps 3;

Qy 5 TTTTGGK-IGKQKQTLVNPGRVNPNGVASLSQAGVPALEKRVTVSVSOPSRNR----- 59
Db 184 TTTLSKEIKAKSGEVVAL-----NDTNTTQATKTKTGAMDSKSTLTISVNSKTTQVLVFT 238

Qy 60 KNYKVQVKIONPTACTANGS 79
Db 239 KQYITTVKQYDSAGTNLEGT 258

RESULT 13
US-09-045-186-2

Sequence 2, Application US/09045186
Patent No. 6087154

GENERAL INFORMATION:

APPLICANT: Baez, Melvyn

TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

STREET: Eli Lilly and Company
CITY: Indianapolis
STATE: Indiana

COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36, 808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-045-186-2

Query Match 10.3%; Score 68.5; DB 3; Length 383;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRYTVSVQPSRNRKRYQVK 67
DB 138 RHQLINPRGWRPNRHHAYGIAVIWLAVALSSLPFLIYQ--VMTDEPFQ----- 186

QY 68 IQNPTACTNAGSCDPSYTRQKXADVTFSFYQSTDEERAFVTELAAL 115
DB 187 -----VTLDAVKDKYVCFDQFSDSHRLSTYTLVLVL 218

RESULT 14
US-08-232-144-4
Sequence 4, Application US/08232144
Patent No. 5571695
GENERAL INFORMATION:
APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
APPLICANT: SHINE, John
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, F19g, Ernst & Kutz
STREET: 555 13th St, N.W., Suite 701-East
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,144
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-107A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-144-4

Query Match 10.3%; Score 68.5; DB 1; Length 384;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRYTVSVQPSRNRKRYQVK 67
DB 138 RHQLINPRGWRPNRHHAYGIAVIWLAVALSSLPFLIYQ--VMTDEPFQ----- 186

QY 68 IQNPTACTNAGSCDPSYTRQKXADVTFSFYQSTDEERAFVTELAAL 115
DB 187 -----VTLDAVKDKYVCFDQFSDSHRLSTYTLVLVL 218

RESULT 15
US-08-555-268A-15
Sequence 15, Application US/08555268A
Patent No. 5958709
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Mary
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,268A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44743-Z/JPM/WAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0526
TELEFAX: (212) 278-0400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-555-268A-15

Query Match 10.3%; Score 68.5; DB 2; Length 384;
Best Local Similarity 25.0%; Pred. No. 7;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRVNPNTN-----GVA---SLSQAGVPALEKRYTVSVQPSRNRKRYQVK 67
DB 138 RHQLINPRGWRPNRHHAYGIAVIWLAVALSSLPFLIYQ--VMTDEPFQ----- 186

Oy 68 IQNPTACTANGSCDPSYTRQKYADVTFSTQYSTDEERAFAVRELAAL 115
Db 187 -----VTLDAIKDKYVCFDQFPSPDSHRLSYTTLALVL 218

Search completed: January 4, 2005, 09:35:44
Job time : 11.3622 secs

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OM protein - protein search, using SW model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-7

Perfect score: 663
Sequence: 1 AKLEVTITGKIGKQKQTLV.....AALLASPLIDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1539051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1539051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications AA.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	132	14	US-10-243-739-24
2	663	100.0	132	14	US-10-244-065-24
3	663	100.0	132	14	US-10-289-454-24
4	663	100.0	132	14	US-10-050-902-256
5	663	100.0	132	14	US-10-050-898-256
6	663	100.0	132	14	US-10-346-190-24
7	663	100.0	132	15	US-10-465-811-15
8	663	100.0	132	15	US-10-289-456-24
9	663	100.0	132	15	US-10-622-064-7
10	663	100.0	132	15	US-10-622-124-18
11	663	100.0	132	16	US-10-622-087-18
12	655	98.8	132	14	US-10-243-739-23
13	655	98.8	132	14	US-10-243-739-26

14	655	98.8	132	14	US-10-244-065-23	Sequence 23, Appl
15	655	98.8	132	14	US-10-244-065-26	Sequence 26, Appl
16	655	98.8	132	14	US-10-289-454-23	Sequence 23, Appl
17	655	98.8	132	14	US-10-289-454-26	Sequence 26, Appl
18	655	98.8	132	14	US-10-050-902-255	Sequence 255, App
19	655	98.8	132	14	US-10-050-902-259	Sequence 259, App
20	655	98.8	132	14	US-10-050-898-255	Sequence 255, App
21	655	98.8	132	14	US-10-050-898-259	Sequence 259, App
22	655	98.8	132	14	US-10-346-190-23	Sequence 23, Appl
23	655	98.8	132	14	US-10-346-190-26	Sequence 26, Appl
24	655	98.8	132	15	US-10-465-811-14	Sequence 14, Appl
25	655	98.8	132	15	US-10-465-811-17	Sequence 17, Appl
26	655	98.8	132	15	US-10-289-456-23	Sequence 23, Appl
27	655	98.8	132	15	US-10-289-456-26	Sequence 26, Appl
28	655	98.8	132	15	US-10-622-064-6	Sequence 6, Appl
29	655	98.8	132	15	US-10-622-064-9	Sequence 9, Appl
30	655	98.8	132	15	US-10-622-124-17	Sequence 17, Appl
31	655	98.8	132	15	US-10-622-087-17	Sequence 17, Appl
32	655	98.8	132	16	US-10-622-087-20	Sequence 20, Appl
33	655	98.8	132	16	US-10-243-739-25	Sequence 25, Appl
34	652	98.3	132	14	US-10-243-739-25	Sequence 25, Appl
35	652	98.3	132	14	US-10-243-739-27	Sequence 27, Appl
36	652	98.3	132	14	US-10-244-065-10	Sequence 10, Appl
37	652	98.3	132	14	US-10-244-065-25	Sequence 25, Appl
38	652	98.3	132	14	US-10-244-065-27	Sequence 27, Appl
39	652	98.3	132	14	US-10-289-454-10	Sequence 10, Appl
40	652	98.3	132	14	US-10-289-454-25	Sequence 25, Appl
41	652	98.3	132	14	US-10-289-454-27	Sequence 27, Appl
42	652	98.3	132	14	US-10-050-902-159	Sequence 159, App
43	652	98.3	132	14	US-10-050-902-257	Sequence 257, App
44	652	98.3	132	14	US-10-050-902-258	Sequence 258, App
45	652	98.3	132	14	US-10-050-902-258	Sequence 258, App

ALIGNMENTS

RESULT 1
US-10-243-739-24
; Sequence 24, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent version 3.1
; SEQ ID NO 24
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-24

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTITGKIGKQKQTLVNPFGVNTNGVASISQGANVPALAEKRTVSVSQPSRRK 60
DB 1 AKLEVTITGKIGKQKQTLVNPFGVNTNGVASISQGANVPALAEKRTVSVSQPSRRK 60
QY 61 NYKVVQKIONPACTANGSCDPSVTRKQYADVTGFTSYSTDEBRAFVTELAALIASPL 120
DB 61 NYKVVQKIONPACTANGSCDPSVTRKQYADVTGFTSYSTDEBRAFVTELAALIASPL 120
QY 121 LIDALDQNPAY 132

Db 121 LIDAIDQLNPA 132

RESULT 2

US-10-244-065-24

Sequence 24, Application US/10244065
Publication No. US2003009668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tissot, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Weijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-24

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4,3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNRK 60
Db 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNRK 60
QY 61 NYKVQVKIONPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTELAALLASPL 120
Db 61 NYKVQVKIONPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPA 132
Db 121 LIDAIDQLNPA 132

RESULT 3

US-10-289-454-24

Sequence 24, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
PRIOR FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/336,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-243
US-10-289-454-24

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4,3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNRK 60
Db 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNRK 60
QY 61 NYKVQVKIONPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTELAALLASPL 120
Db 61 NYKVQVKIONPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPA 132
Db 121 LIDAIDQLNPA 132

RESULT 4

US-10-050-902-256

Sequence 256, Application US/10050902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Seibel, Peter
APPLICANT: Plosek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US/10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 256
LENGTH: 132
TYPE: PRT
ORGANISM: Qb 243
US-10-050-902-256

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4,3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNRK 60
Db 1 AKLEVTYLGKIGDKQKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVQSPSRNRK 60
QY 61 NYKVQVKIONPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTELAALLASPL 120
Db 61 NYKVQVKIONPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPA 132
Db 121 LIDAIDQLNPA 132


```

RESULT 5
US-10-050-898-256
; Sequence 256, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 256
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Db 243
US-10-050-898-256

Query Match      100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASISQAGAVPALKRTVTSVSOSSRRK 60
Db      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASISQAGAVPALKRTVTSVSOSSRRK 60
Qy      61 NYKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

RESULT 6
US-10-346-190-24
; Sequence 24, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pellucidoli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

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; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Db 243
US-10-346-190-24

Query Match      100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASISQAGAVPALKRTVTSVSOSSRRK 60
Db      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASISQAGAVPALKRTVTSVSOSSRRK 60
Qy      61 NYKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

RESULT 7
US-10-465-811-15
; Sequence 15, Application US/10465811
; Publication No. US2004000538A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 243 mutant
US-10-465-811-15

Query Match      100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASISQAGAVPALKRTVTSVSOSSRRK 60
Db      1 AKLEVTYTGKIGKQKQTLVLPNGVPTNGVASISQAGAVPALKRTVTSVSOSSRRK 60
Qy      61 NYKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

RESULT 8
US-10-289-456-24
; Sequence 24, Application US/10289456

```

Publication No. US20040033211A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Q-beta 243 mutant
US-10-289-456-24

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
DB 1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
QY 61 NYKVQVQIONPTACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVRELAALASPL 120
DB 61 NYKVQVQIONPTACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVRELAALASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 9

US-10-622-064-7
Sequence 7, Application US/10622064
Publication No. US20040059094A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrick F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,575
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 243 mutant
US-10-622-064-7

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
DB 1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60

DB 1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
QY 61 NYKVQVQIONPTACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVRELAALASPL 120
DB 61 NYKVQVQIONPTACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVRELAALASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 10

US-10-622-124-18
Sequence 18, Application US/10622124
Publication No. US20040076645A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Fuhurija, Alma
TITLE OF INVENTION: Ghrelin-Carrier Conjugates
FILE REFERENCE: 1700.0340001
CURRENT APPLICATION NUMBER: US/10/622,124
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,638
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 243 mutant
US-10-622-124-18

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
DB 1 AKLEVTTLGKIGDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
QY 61 NYKVQVQIONPTACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVRELAALASPL 120
DB 61 NYKVQVQIONPTACTANGSCDPSVTRQKXADVTFSFTQYSTDERAFVRELAALASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 11

US-10-622-087-18
Sequence 18, Application US/10622087
Publication No. US20040141984A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tissot, Alain
APPLICANT: Ottmann, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Scaufenbiel, Matthias
APPLICANT: Frey, Peter
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,639
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/470,432
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin version 3.2
SEQ ID NO 18

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; LENGTH: 132
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 243 mutant
US-10-622-087-18

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Query Match	100.0%;	Score 663;	DB 16;	Length 132;
Best Local Similarity	100.0%;	Pred. No. 4.3e-66;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy 1 AKLEVTTLGKIGKDGKQTLVLRNGVNPINGVASLSQAGVPALEKRVTVSVSQPSRNRK 600

Db 1 AKLEVTTLGKIGKDGKQTLVLRNGVNPINGVASLSQAGVPALEKRVTVSVSQPSRNRK 600

QY 61 NYKVQVKIQNPCTACTGNGSCPSVTRQKADYTFSEFOYSTDEERAFVETELAAALLSPL 120

Db 61 NYKVQVKIQNPCTACTGNGSCPSVTRQKADYTFSEFOYSTDEERAFVETELAAALLSPL 120

QY	121	L1DAIDQLNPAY	132
Db	121	L1DAIDQLNPAY	132

RESULT 12
US-10-243-739-23

```

: GENERAL INFORMATION:
: APPLICANT: Bachmann, Martin F.
: APPLICANT: Storni, Tazio
: APPLICANT: Lechner, Franziska
: TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
: TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
: FILE REFERENCE: 1700_0210001
: CURRENT APPLICATION NUMBER: US/10/243,739
: CURRENT FILING DATE: 2002-09-16
: PRIOR APPLICATION NUMBER: 60/318,967
: PRIOR FILING DATE: 2001-09-14
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 23
: LENGTH: 132
: TYPE: PRT
: ORGANISM: Bacteriophage Q-beta
: US-10-243-739-23

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Query Match	98.8%	Score 655;	DB 14;	Length 132;
Best Local Similarity	98.5%	Pred. No. 3.4e-65;		
Matches 130; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0

Oy

1 AKLETTTLGKIGDKQTVLNRGVNPNGVASLSQAQAVPALEKRVTYSVSQPBRNRK 600
||||| : |||||
Dd

1 AKLETTLGNIRGDQTVLNRGVNPNGVASLSQAQAVPALEKRVTYSVSQPBRNRK 600

QY 61 NKKVQVKIQNPACTANNGSCPSVTEQOKADYTSFQYSTETBERAFRTETLAAILASPL 120
 61 NKKVQVKIQNPACTANNGSCPSVTEQOKADYTSFQYSTETBERAFRTETLAAILASPL 120
 Db 61 NKKVQVKIQNPACTANNGSCPSVTEQOKADYTSFQYSTETBERAFRTETLAAILASPL 120

QY	121	LIDAIDQLNPAY	132
Db	121	LIDAIDQLNPAY	132

RESULT 13
US-10-243-739-26

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; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornl, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of

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: TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
:
: FILE REFERENCE: 1700.0210001
:
: CURRENT APPLICATION NUMBER: US/10/243,739
:
: CURRENT FILING DATE: 2002-09-16
:
: PRIOR APPLICATION NUMBER: 60/318,967
:
: PRIOR FILING DATE: 2001-09-14
:
: NUMBER OF SEQ. ID NOS: 73
:
: SOFTWARE: PatentIn version 3.1
:
: SEQ. ID NO: 26
:
: LENGTH: 132
:
: TYPE: PR1
:
: ORGANISM: Bacteriophage Q-beta
:
: US-10-243-739-26

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Query Match	98.8%	Score 655;	DB 14;	Length 132;
Best Local Similarity	98.5%	Pred. No. 3.4e-65;		
Matches 130; Conservative	1;	Mismatches	1;	Indels 0; Gaps 0

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Qy      1 AKLEVTYTGKIGKDGKQTLVLPNGVAPPTNGVASLSQAGAVPALEKRVTVSVSQPERNRK 60
        |||||:|||||
Db      1 AKLEVTYTGKIGKDGQTLVLPNGVAPPTNGVASLSQAGAVPALEKRVTVSVSQPERNRK 60

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Qy 61 NYKQVKIQNPCTANGSCDPSVTRQKADVTFSTQYSIDDEBRAVRETELALLASP.L 120C
Db 61 NYKQVKIQNPCTANGSCDPSVTRQKADVTFSTQYSIDDEBRAVRETELALLASP.L 120C

QY	121	L1DA1DQLNPA	132
Db	121	L1DA1DQLNPA	132

RESULT 14
US-10-244-065-23

```

: GENERAL INFORMATION:
: APPLICANT: Bachmann, Martin F.
: APPLICANT: Stormi, Tazio
: APPLICANT: Mauret, Patrick
: APPLICANT: Tissot, Alain
: APPLICANT: Schwarz, Katrin
: APPLICANT: Meljerink, Edwin
: APPLICANT: Lipowsky, Gerd
: APPLICANT: Pumpens, Paul
: APPLICANT: Cielems, Indulis
: APPLICANT: Rehofa, Regina
: TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
: TITLE OR INVENTION: Method of Preparation and Use
: PRIORITY REFERENCE: 1700.0220001
: CURRENT APPLICATION NUMBER: US/10/244,065
: CURRENT FILING DATE: 2002-09-16
: PRIOR APPLICATION NUMBER: 60/374,145
: PRIOR FILING DATE: 2002-04-22

```

PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1

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;
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
;

```

Query Match	98.8%	Score 655;	DB 14;	Length 132;
Best Local Similarity	98.5%	Pred. No. 3.4e-65;		

Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIQOLNPAY 132

Db 121 LIDAIQOLNPAY 132

RESULT 15
US-10-244-065-26

/ Sequence 26, Application US/10244065
/ Publication No. US2003009668A1

/ GENERAL INFORMATION:

/ APPLICANT: Bachmann, Martin F.

/ APPLICANT: Storni, Tazio

/ APPLICANT: Maurer, Patrick

/ APPLICANT: Tissot, Alain

/ APPLICANT: Schwarz, Katrin

/ APPLICANT: Meijerink, Edwin

/ APPLICANT: Lipowsky, Gerard

/ APPLICANT: Pumpens, Paul

/ APPLICANT: Clejens, Indulis

/ APPLICANT: Renhofa, Regina

/ TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particl

/ FILE REFERENCE: 1700.0220001

/ CURRENT APPLICATION NUMBER: US/10/244,065

/ PRIOR FILING DATE: 2002-09-16

/ PRIOR FILING DATE: 2002-04-22

/ PRIOR APPLICATION NUMBER: 60/318,994

/ PRIOR FILING DATE: 2001-09-14

/ NUMBER OF SEQ ID NOS: 73

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 26

/ LENGTH: 132

/ TYPE: PR

/ ORGANISM: Bacteriophage Q-beta

US-10-244-065-26

Query Match 98.8%; Score 655; DB 14; Length 132;

Best Local Similarity 98.5%; Pred. No. 3.4e-65;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLETVTLKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSRNK 60

Db 1 AKLETVTLKIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTYSVQPSRNK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDERAFVTEIAALLASPL 120

Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKYADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIQOLNPAY 132

Db 121 LIDAIQOLNPAY 132

Search completed: January 4, 2005, 09:41:22

Job time : 33.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-7

Perfect score: 663

Sequence: 1 AKLETVTLLGKIGDKGKQTLV.....ALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	652	98.3	132	1	VCBPOB
2	537.5	81.1	331	2	S01964
3	116	17.5	131	1	VCBPP1
4	90.5	13.7	530	2	S22340
5	88.5	13.3	540	2	T00646
6	84.5	12.7	529	2	S24231
7	84.5	12.7	529	2	A43505
8	84.5	12.7	529	2	AC1100
9	81	12.2	432	2	T31660
10	80.5	12.1	528	2	S22341
11	80.5	12.1	1502	1	RGBYH1
12	79.5	12.0	136	2	C98221
13	79.5	12.0	136	2	AE3065
14	79	11.9	282	2	A10186
15	78.5	11.8	191	2	H90078
16	78.5	11.8	830	2	S57537
17	78.5	11.8	1052	2	C64221
18	78.5	11.8	1861	2	T13845
19	76	11.5	1461	2	E90696
20	76	11.5	1461	2	A85547
21	75.5	11.4	1097	2	AD2572
22	74.5	11.2	130	1	VCBPPR
23	74.5	11.2	161	4	I55480
24	74.5	11.2	340	2	S18650
25	74.5	11.2	340	2	A42008
26	74	11.2	130	1	A46324
27	73.5	11.1	520	1	ACMSD1
28	73.5	11.1	601	2	A55921
29	73.5	11.1	719	2	T39271

30	73	11.0	130	1	VCBPGA	coat protein - pha
31	73	11.0	243	1	VHVUPT	nucleocapsid prote
32	73	11.0	430	2	G88884	protein K09B11.10
33	73	11.0	463	2	S00676	translation elonga
34	72.5	10.9	458	2	T49114	hypothetical prote
35	72.5	10.9	654	2	S69673	SAC7 protein - yea
36	72	10.9	366	2	F70618	probable pntAA pro
37	72	10.9	399	1	A43685	polymerase-associ
38	71	10.7	248	2	A86786	conserved hypochet
39	71	10.7	376	2	C84316	hypothetical prote
40	70.5	10.6	129	1	VCBPP2	coat protein - pha
41	70.5	10.6	129	1	VCBPP7	coat protein - pha
42	70.5	10.6	129	1	VCBPPR	coat protein - pha
43	70	10.6	434	2	S72430	transcription elon
44	70	10.6	434	2	D88305	protein R03D7.4 [i
45	70	10.6	694	2	P97279	TPR-repeat-contain

ALIGNMENTS

RESULT 1
VCBPOB
coat protein - phase Q-beta
C/Species: phage Q-beta
C/Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004
C/Accession: A92240; A92221; A92088; A04224
R/Becarmig, C.; Sastry, P.A.; Biller, M.A.
J. Biol. Chem. 253, 8390-8399, 1978
A/Title: Determination of the first half of the coat protein cistron of bacteriophage Q
A/Reference number: A92240; PMID:79048469; PMID:361741
A/Accession: A92240
A/Molecule type: mRNA
A/Residues: 1-80 <ESCS>
A/Cross-references: UNIPROT:P03615
J. Stoll, E.; Wilson, K.J.; Reiser, J.; Weisemann, C.
R. Biol. Chem. 252, 990-993, 1977
A/Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.
A/Reference number: A92221, PMID:7118576; PMID:838709
A/Accession: A92221
A/Molecule type: protein
A/Residues: 1-60 <STO>
R/Malta, T.; Konigsberg, W.
J. Biol. Chem. 246, 5003-5024, 1971
A/Title: The amino acid sequence of the Qbeta coat protein.
A/Reference number: A92088; PMID:7128580; PMID:5570434
A/Molecule type: protein
A/Residues: 1-21, 'D', '23-55, 57-132 <MAI>
C/Superfamily: phage GA coat protein

Query Match
Best Local Similarity 98.3%; Score 652; DB 1; Length 132;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKLETVTLLGKIGDKGKQTLVLRGVPNTGVSLSQAGVPALEKRVTVSQPSNRK 60
Db 1 NYKVQYKIQNPACTANGSCDPSTROAVADVTFSTQYSTDBERAFVETLAALASPL 120
QY 61 NYKVQYKIQNPACTANGSCDPSTROAVADVTFSTQYSTDBERAFVETLAALASPL 120
Db 61 NYKVQYKIQNPACTANGSCDPSTROAVADVTFSTQYSTDBERAFVETLAALASPL 120
QY 121 LIDAIIDQNPAY 132
Db 121 LIDAIIDQNPAY 132

RESULT 2
S01964
readthrough protein - phase SP
C/Species: phage SP
C/Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 09-Jul-2004

R/naas, A.; Jumasov, M.; Kleric, U. Blochim. Biophys. Acta 1130, 81-84, 1992

A1:Title: listeriolysin genes: complete sequence of ilo from *Listeria Ivanovi* and of lsc

A:Reference number: S22340; MUID:92182018; PMID:143752

A1:Accession: S24231
A1:Status: nucleic acid sequence not shown; translation not shown
A1:Molecule type: DNA

A:Residues: 1-529 <RAS>
A:Cross-references: UNIPROT:P13128; EMBL:X60035; NID:g44110; PID:CAA42639.1; PID:g44112
A:Experimental source: strain 12067, serotype 4b
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C:Genetics:
A:Gene: hlyA
C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-529/Product: listeriolysin O #status predicted <MAT>

Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.1;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGRKOTLVL-----NPRGVNPTNGVASISQGA-----VPALERKV 48
DB 93 KDGRNYIVVEKKKKSINQNNADIQVNAISSITFGALVKANSELVENQPDVLPYKRBSL 152
QY 49 TVSVQSPSRNRKNYQVQKIQNPACTANGSCDPSVTR-----OKYADVTFSSFTQYSTD 102
DB 153 TLTSIDLPGMTQNDKNIYVK--NATKSNVNNNAVNTLVERNNEKYAAYPRVVS---AKIDYD 207
QY 103 EERAFVTELLA 114
DB 208 DEMAYSESOLIA 219

RESULT 7
A43505
Listeriolysin O precursor - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 21-Oct-1992 #sequence revision 21-Oct-1992 #text_change 09-Jul-2004
C:Accession: A43505; S05306; A47606; S12400; A61079
R:Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Saurey
Infect. Immun. 56, 766-772, 1988
A:Title: Expression in *Escherichia coli* and sequence analysis of the listeriolysin O de
A:Reference number: A43505; PMID:88153053; PMID:3126142
A:Accession: A43505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <MEN>
A:Cross-references: UNIPROT:P13128; GB:M24199; NID:g149652; PID:AAA03018.1; PID:g149653
A:Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R:Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A:Title: Nucleotide sequence of the listeriolysin gene from a *Listeria monocytogenes* ser
A:Reference number: S05306; PMID:89366684; PMID:2505236
A:Accession: S05306
A:Molecule type: DNA
A:Residues: 1-529 <DOM>
A:Cross-references: EMBL:X15127; NID:g44106; PID:CAA33223.1; PID:g44107
A:Experimental source: strain EGD
A:Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R:Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cossart, P.
Infect. Immun. 55, 3225-3227, 1987
A:Title: Identification of the structural gene encoding the SH-activated hemolysin of *Li*
A:Reference number: A47606; PMID:88057627; PMID:2824384
A:Accession: A47606
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 413-480 <ME2>
A:Cross-references: GB:M29171
R:Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A:Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtain
A:Reference number: S12400; PMID:91211627; PMID:1965218
A:Accession: S12400
A:Molecule type: DNA
A:Residues: 483-493 <MIC>
A:Experimental source: strain L028, serotype 1/2c
C:Genetics:
A:Gene: hlyA; hlyB

C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-529/Product: listeriolysin O #status predicted <MAT>

Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.1;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGRKOTLVL-----NPRGVNPTNGVASISQGA-----VPALERKV 48
DB 93 KDGRNYIVVEKKKKSINQNNADIQVNAISSITFGALVKANSELVENQPDVLPYKRBSL 152
QY 49 TVSVQSPSRNRKNYQVQKIQNPACTANGSCDPSVTR-----OKYADVTFSSFTQYSTD 102
DB 153 TLTSIDLPGMTQNDKNIYVK--NATKSNVNNNAVNTLVERNNEKYAAYPRVVS---AKIDYD 207
QY 103 EERAFVTELLA 114
DB 208 DEMAYSESOLIA 219

RESULT 8
AC1100
Listeriolysin O precursor [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1100
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baghero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Falhi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schueeler, T.; Simoes, N.; Trierer, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; PMID:11679669
A:Accession: AC1100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <GLA>
A:Cross-references: UNIPROT:P13128; GB:NC_003210; PID:CAD00729.1; PID:g16409567; GSPDB:C
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: hly
C:Superfamily: dipeptide transport protein

Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.1;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDGRKOTLVL-----NPRGVNPTNGVASISQGA-----VPALERKV 48
DB 93 KDGRNYIVVEKKKKSINQNNADIQVNAISSITFGALVKANSELVENQPDVLPYKRBSL 152
QY 49 TVSVQSPSRNRKNYQVQKIQNPACTANGSCDPSVTR-----OKYADVTFSSFTQYSTD 102
DB 153 TLTSIDLPGMTQNDKNIYVK--NATKSNVNNNAVNTLVERNNEKYAAYPRVVS---AKIDYD 207
QY 103 EERAFVTELLA 114
DB 208 DEMAYSESOLIA 219

RESULT 9
T31660
Hypothetical protein COS41.6 - sea squirt (*Ciona intestinalis*)
C:Species: *Ciona intestinalis*
C:Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31660
R:Bird, A.P.; Clark, V.; Jones, S.J.; Leigeb, S.; Dobson, R.; Tweedle, S.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z21049
A:Accession: T31660

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-432 <BIR>
A:Cross-references: UNIPROT:P51584; EMBL:Z63760; NID:e1014349; PID:e289996; PIDN:CA00605
A:introns: 180/2; 212/1; 229/3

Query Match 12.2%; Score 81; DB 2; Length 432;
Best Local Similarity 28.3%; Pred. No. 3.7;
Matches 32; Conservative 17; Mismatches 46; Indels 18; Gaps 6;

QY 4 ETVTLKIGKDGKQTLVLRGVNPTNGVSLSQAGVPALEKRVTVSVSQPSRRKNTK 63
DB 242 DISSEGEVLTKDGGNLAENP---TPSNAARELOESVASEVLETVVKSALQ-EQDSAYR 297
QY 64 VQVKIKNPAPAC-TANGSC-----DPSVTRKQYAD-----VTFSTQYSTDE 103
DB 298 KR-NPQNAAPACPNRNGNCVSTNSNKTPTNDSKIEIVNSDNTTDEDTQIDTNE 349

RESULT 10

S22341
Ivanolysin precursor - Listeria ivanovii
C:Species: Listeria ivanovii
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S22341; S36683
R:Haas, A.; Dumbeky, M.; Krefc, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A:Title: Listeriolysin genes: complete sequence of 110 from Listeria ivanovii and of 160
A:Reference number: S22340; M01D:92182018; PMID:1543752
A:Accession: S22341
A:Molecule type: DNA
A:Residues: 1-528 <HMS>
A:Cross-references: UNIPROT:P31831; EMBL:X60461
A>Note: the authors translated the codon ACA for residue 331 as Val
R:Krefc, J.
submitted to the EMBL Data Library, July 1991
A:Reference number: S36683
A:Accession: S36683
A:Molecule type: DNA
A:Residues: 1-319, 'T', 321-528 <KRE>
A:Cross-references: EMBL:X60461
C:Genetics: 110
A:Gene: 110
C:Superfamily: dipeptide transport protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-528/Product: Ivanolysin #status predicted <MAT>

Query Match 12.1%; Score 80.5; DB 2; Length 528;
Best Local Similarity 22.0%; Pred. No. 5.3;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 KDKGKTLV-----NRGVNPTNGVSLSQAG-----VPALEKRY 48
DB 92 KEENQYIVAEKKKKSINQNNADIQVINSLSLTPGALVANSSELVENQPDVLPVKRDSV 151
QY 49 TVSVSQPSRRKRVKQVKNPACTANGSCDPSVTR-----QKTVDTFSTQYSTD 102
DB 152 TSLIDLP--GMVNDHNEIVQNKATKSNINDGVNLTVDNRNNKXSEKPNIS---AKIDVD 206
QY 103 EERRAVTELLAA 114
DB 207 QEMAYSESQVVA 218

RESULT 11

RGVH1
CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein 1672.1; protein YLR256w; regulatory protein CYP1; regulatory
C:Species: Saccharomyces cerevisiae
C>Date: 30-Sep-1991 #sequence_revision 23-Feb-1996 #text_change 12-Nov-1999
C:Accession: S59400; A31312; S15447; S05804; S15446
R:Johnson, D.

submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9672.

A:Reference number: S59386
A:Accession: S59400
A:Molecule type: DNA

A:Residues: 1-1502 <JCH>
A:Cross-references: EMBL:U20865; NID:g662330; PIDN:AAB67387.1; PID:g662331; GSPDB:GN0001;
A:Experimental source: strain S288C (AB972)
R:Pfeiffer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
Cell 56, 291-301, 1989

A:Title: Functional dissection and sequence of yeast HAP1 activator.

A:Reference number: A31312; M01D:89106221; PMID:2643482

A:Accession: A31312

A:Molecule type: DNA

A:Residues: 1-144, 'I', 146-322, 'R', 324-454, 'N', 456-507, 'W', 509-586, 'K', 588-882, 'N', 884-955
A:Cross-references: EMBL:U03152; NID:g171645; PIDN:AAA34662.1; PID:g171646

R:Crenot, F.; Verdier, J.; Galet, M.; Slonimski, P.P.
U. Mol. Biol. 204, 263-276, 1988

A:Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall

A:Reference number: S15447; M01D:89125585; PMID:2851558

A:Accession: S15447

A:Molecule type: DNA

A:Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADPIME' <CREI>

A:Cross-references: EMBL:X13793

A>Note: the sequence is from mutant CYP1-18

C:Genetics: 12R

A:Gene: SGD:HAP1; CYP1; MIPS:YLR256w

A:Cross-references: SGD:S0004246; MIPS:YLR256w

A:Map position: 12R

C:Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology

C:Keywords: DNA binding; heme binding; transcription regulation; zinc finger

F:1-148/Domain: DNA binding #status predicted <DNA>

F:59-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>

F:64-84/Region: zinc finger CCCC motif

F:177-189/Region: glutamine-rich

F:245-445/Domain: heme binding #status predicted <HEM>

F:299-304, 323-328, 347-352, 373-378, 388-394, 415-420/Region: 6-residue repeats

F:1308-1481/Domain: activation element #status predicted <ACT>

F:1388-1481/Region: acidic

Query Match 12.1%; Score 80.5; DB 1; Length 1502;
Best Local Similarity 20.6%; Pred. No. 18;
Matches 35; Conservative 30; Mismatches 42; Indels 63; Gaps 7;

QY 23 PRGVN--PTNGVSL-----SQAGVPALEKRVTVSVS 53
DB 1278 PRGISPKPNSGLSSVQPLSSFSMNQNGTTPVPSLNTTSQWGLSLDRITNQIN 1337
QY 54 QPSRR-KNYKQVKNP-----TACTANGSCP 82
DB 1338 LPDPSRDEAFDMSIKQMTPTSAFNNANTTIPSTLNGMNNMGAGTANTDTANGSALS 1397
QY 83 SVTRKQYADV-TFSFTQYSTD--ERRAVTELLAALASP-TLIDALDQIN 129
DB 1398 TLTSFGSDLASNSATQKPDLEFLMONGSNFGLMINSLSVEVVGIV 1447

RESULT 12

C98221
hypothetical protein AGR_L1428 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: C98221
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; M01D:21608551; PMID:11743194
A:Accession: C98221
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q8U8F3; GB:AE007870; PIDN:AAK89293.1; PID:g15159127; GSPDB:GN

C:Genetics:
A:Gene: AGR_L_1428
A:Map position: linear chromosome

Query Match 12.0%; Score 79.5; DB 2; Length 136;
Best Local Similarity 25.4%; Pred. No. 1.4;
Matches 30; Conservative 15; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGDGKQTLVLPNGVPTNGVASLSQAGV-----PALEKRVTVSVQSPSRNR 59
DB 3 ISKDKQTESADPHMIEMVTGTISTLVAMFGWIAIDYRYSPEBARPEIAVTVGEQGT 62
QY 60 KNYKVQVXIQNFTACTA-----NGSCDPSVTRQKADVTFSF-TQYSTDEBARFVTE 111
DB 63 GQYRVKFAIHNLSMTTAAQVNVGRDLEQNGASPENADVTFDYVASESKDNGTLFFRSD 120

RESULT 13

AE3065
conserved hypothetical protein Atu4139 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE3065
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyaev, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3065
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q8U8R3; GB:AE0086683; PIDD:AL44939.1; PID:g17742593; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4139
A:Map position: linear chromosome

Query Match 12.0%; Score 79.5; DB 2; Length 136;
Best Local Similarity 25.4%; Pred. No. 1.4;
Matches 30; Conservative 15; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGDGKQTLVLPNGVPTNGVASLSQAGV-----PALEKRVTVSVQSPSRNR 59
DB 3 ISKDKQTESADPHMIEMVTGTISTLVAMFGWIAIDYRYSPEBARPEIAVTVGEQGT 62
QY 60 KNYKVQVXIQNFTACTA-----NGSCDPSVTRQKADVTFSF-TQYSTDEBARFVTE 111
DB 63 GQYRVKFAIHNLSMTTAAQVNVGRDLEQNGASPENADVTFDYVASESKDNGTLFFRSD 120

RESULT 14

AI0186
Probable iron-siderophore transport system, ATP-binding component YPO1533 [imported] - Y
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AI0186
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Stimmendorf, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AI0186
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <KUR>
A:Cross-references: UNIPROT:Q8ZF20; GB:AL590842; PIDD:CA090356.1; PID:g15979576; GSPDB:C
C:Genetics:
A:Gene: YPO1533

C:Superfamily: inner membrane protein malK; ATP-binding cassette homology

Query Match 11.9%; Score 79; DB 2; Length 282;
Best Local Similarity 22.0%; Pred. No. 3.6;
Matches 27; Conservative 37; Mismatches 45; Indels 14; Gaps 5;

QY 13 KDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVQSPSRNRKNYKVQVXIQNFT 72
DB 49 KNGAFSVIIGPNCCKSKTLRLRS---LTPONGSIRLDQ--QDIOHYKAKVFARQLS 102
QY 73 ACTANGSCDPSVT-----ROKADVTFSFTQYSTDEBARFVTEALALASPLLDIDA 126
DB 103 LLSQASISSETITVTDVLSRGRYHQSF-FHWSIEDER-IYKAALSAVNESLIVQGRVS 160
QY 127 QLN 129
DB 161 ELS 163

RESULT 15

H90078
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90078
R:Kuruda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9756; MUID:21311952; PMID:11418146
A:Accession: H90078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <KUR>
A:Cross-references: UNIPROT:Q99QUS; GB:BA000018; PIDD:g13702654; PIDD:BA843794.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2488

Query Match 11.8%; Score 78.5; DB 2; Length 191;
Best Local Similarity 24.1%; Pred. No. 2.6;
Matches 27; Conservative 24; Mismatches 50; Indels 11; Gaps 3;

QY 6 VTLGKIGDKQTLVLPNGVPTNGVASLSQAGV-----GAVPALEKRVTVSVQSPSRNR 59
DB 1 MTLPRIGKPA--TRALNQGITYTLEAVSQYTKSSLMENHGVGP---KAISILEQALFQHQ 55
QY 60 KNYKVQVXIQNFTACTANGSCDPSVTRQKADVTFSFTQYSTDEBARFVTE 111
DB 56 LHFKTEVQSLPFLKLTGVSCHHAPKQOMIDFIVATLADIELRLSLVTTT 107

Search completed: January 4, 2005, 09:17:30
Job time : 9.03224 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-7

Perfect score: 663
Sequence: 1 AALETYLTKIGKDGKQTLV.....AALIASPLIDAIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652	98.3	132	1	COAT_BPOBE
2	652	98.3	132	2	AAM33126
3	652	98.3	329	2	081RE1
4	652	98.3	329	2	AAA16663
5	565	85.2	133	2	09TOR9
6	565	85.2	329	2	064307
7	545	82.2	133	2	09TOS0
8	545	82.2	329	2	064303
9	537.5	81.1	132	1	COAT_BPSP
10	537.5	81.1	331	1	VAI_BPSP
11	497.5	75.0	132	2	09TOR8
12	497.5	75.0	330	2	064310
13	116	14.0	131	1	COAT_BPPRR
14	93	14.0	473	1	08VDC2
15	90.5	13.7	530	1	TACY_LISSE
16	90.5	13.7	530	2	AAP97361
17	88.5	13.3	540	2	048683
18	84.5	12.7	529	1	TACY_LISMF
19	84.5	12.7	529	1	TACY_LISMO
20	84.5	12.7	529	2	0915B9
21	84.5	12.7	529	2	06B9A2
22	84.5	12.7	529	2	06B9A2
23	84.5	12.7	529	2	06B9A2
24	84.5	12.7	529	2	06B9A2
25	84.5	12.7	529	2	06B9A2
26	84.5	12.7	529	2	06B9A2
27	84.5	12.7	529	2	06B9A2
28	84.5	12.7	529	2	06B9A2
29	84.5	12.7	529	2	06B9A2
30	84.5	12.7	529	2	06B9A2
31	84.5	12.7	529	2	AAT03000

32	84	12.7	1624	2	Q9V3K8	Q9V3K8 drosophila
33	84	12.7	1637	2	Q95RU8	Q95RU8 drosophila
34	82.5	12.4	461	2	Q7PP73	Q7PP73 anopheles g
35	82	12.4	336	2	Q8RRP3	Q8RRP3 methanosarc
36	82	12.4	512	2	Q6HGA7	Q6HGA7 bacillus th
37	81.5	12.3	608	2	Q84H79	Q84H79 rhodococcus
38	81	12.2	432	2	P91584	P91584 clona inter
39	80.5	12.1	528	1	TACY_LISIV	P31831 listeria iv
40	80.5	12.1	528	2	Q6R6D9	Q6R6D9 listeria iv
41	80.5	12.1	528	2	AAR97343	AAR97343 listeria
42	80.5	12.1	1502	1	CYPL_YEAST	P12351 saccharomyc
43	79.5	12.0	136	2	Q7CU57	Q7CU57 agrobacteri
44	79.5	12.0	136	2	Q8U8F3	Q8U8F3 agrobacteri
45	79	11.9	282	2	Q8ZFF20	Q8ZFF20 yersinia pe

ALIGNMENTS

RESULT 1
COAT_BPOBE STANDARD; PRT; 132 AA.
ID COAT_BPOBE
AC P03615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coar protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirulins.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Chelens I., Drellima D., Dieters A., Bauman V.,
Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmis C., Sastry P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
bacteriophage Q-beta as an application of a mapping procedure for RNA
fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maiz T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundale M., Valgard K., Liljas L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M99039; AAA16662.1; -.
DR EMBL; V00643; CAA23992.1; -.
DR PIR; A92340; VCBPOB.
DR PDB; 1QBE; X-ray; A/B/C=1-133.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
DR 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
KM INIT MET 0 0
FT CONFLICT 22 22 N -> D (in Ref. 4).
FT CONFLICT 56 56 Missing (in Ref. 4).
FT STRAND 6 9
FT TURN 13 14
FT STRAND 18 27
FT TURN 28 31
FT STRAND 32 36
FT HELIX 42 44
FT STRAND 47 53
FT STRAND 56 58
FT TURN 57 58
FT STRAND 59 59
FT STRAND 62 74
FT STRAND 83 96
FT TURN 98 99
FT HELIX 102 117
FT HELIX 119 126
FT TURN 127 127
SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 98.3%; Score 652; DB 1; Length 132;
Best Local Similarity 98.5%; Pred. No. 2.4e-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKLETVTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSRRNK 60
DB 1 AKLETVTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSRRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 2
AAM33126 PRELIMINARY; PRT; 133 AA.
ID AAM33126;
AC AAM33126;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievivirus; Altolievirus subgroup III.
OK NCBI_TaxID=12009;
RN NCBI_TaxID=12009;
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes.";
RL BMC Evol. Biol. 3:24-24(2003).
DR EMBL; AY099114; AAM33126.1; -.
KW Coat protein.
SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.3%; Score 652; DB 2; Length 133;
Best Local Similarity 98.5%; Pred. No. 2.4e-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 AKLETVTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSRRNK 60
DB 2 AKLETVTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSRRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIDQLNPAY 132
DB 122 LIDAIDQLNPAY 133

RESULT 3
Q8LTEL1 PRELIMINARY; PRT; 329 AA.
ID Q8LTEL1;
AC Q8LTEL1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE A1 read-through protein (A1 protein).
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievivirus.
OK NCBI_TaxID=12009;
RN NCBI_TaxID=12009;
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes.";
RL BMC Evol. Biol. 3:24-24(2003).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clelens I., Dreilima D., Dislers A., Baumanns V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; AY099114; AAM33127.1; -.
DR EMBL; M99039; AAA16663.1; -.
DR HSP; P03615; 1QBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Levi_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.3%; Score 652; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 7e-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKLETVTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSRRNK 60
DB 2 AKLETVTLGKIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSRRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIDQLNPAY 132
DB 122 LIDAIDQLNPAY 133

RESULT 4
AAA16663 PRELIMINARY; PRT; 329 AA.
ID AAA16663;
AC AAA16663;
DT 02-MAR-2004 (TREMBlrel. 27, Created)

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DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae.
RN NCB1_Taxid=12009;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielesns I., Dreilima D., Dielers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; M99039; AAA16663.1; -.
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.3%; Score 652; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 76-55;
Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AKLEVTYTLKIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLEVTYTLNIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 120
DB 62 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
ID Q9TOR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae.
RN NCB1_Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBD databases.
DR EMBL; AF059242; AAC14699.1; -.
DR HSSP; P03615; 10BE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 85.2%; Score 565; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 26-46;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTYTLKIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLEVTYTLNIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 120
DB 62 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

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Query Match 85.2%; Score 565; DB 2; Length 133;
Best Local Similarity 83.3%; Pred. No. 6.9e-47;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTYTLKIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLEVTYTLNIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 120
DB 62 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae.
RN NCB1_Taxid=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBD databases.
DR EMBL; AF059242; AAC14700.1; -.
DR HSSP; P03615; 10BE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 85.2%; Score 565; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 26-46;
Matches 110; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLEVTYTLKIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 60
DB 2 AKLEVTYTLNIGDKGQTLVLPNGVNPPTNGVSLSGAGVPALEKRVTVSVSOPSRRNK 61
QY 61 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 120
DB 62 NKVQVQKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDEBRALVTELAALASP 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

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RESULT 7
Q9T0S0 PRELIMINARY; PRT; 133 AA.
ID Q9T0S0;
AC Q9T0S0;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
RT "Secondary structure model for the last two domains of single-stranded RNA phage Q beta."
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Coat protein. M11.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
OC NCB1_TaxID=74336;
RX NCB1_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA. Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF052431; AAC06250.1; --
DR HSSP: P03615; 1QBE.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
DR Coat protein.
KW SEQUENCE 133 AA; 14198 MW; 098722E3C6CA255 CRC64;
SQ
Query Match 82.2%; Score 545; DB 2; Length 133;
Best Local Similarity 80.3%; Pred. No. 6e-45;
Matches 106; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
QY 1 AKLEVTYLGKIGKDGQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 AKLQATLTLSGIRKGGVTLDPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRRNK 61
QY 61 NYKVQYKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBAFVTELAALIASPL 120
DB 62 NYKVQYKIQNPCTSGTCDPSVTRSAVSDFTSFTQYSTVERALVRETELQALLADPM 121
QY 121 LIDAIDQLNPAY 132
DB 122 LVNAIDNLNPAY 133
RESULT 8
Q64303 PRELIMINARY; PRT; 329 AA.
ID Q64303;
AC Q64303;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
RT "Secondary structure model for the last sequence update"
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
OC NCB1_TaxID=74336;
RX NCB1_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA. Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF052431; AAC06251.1; --
DR HSSP: P03615; 1QBE.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF01819; Lev1_coat; 1.
DR PROSITE: PS00030; RNA_RNP_1; UNKNOWN 1.
DR SEQUENCE 329 AA; 35893 MW; 3E3CD821E625F4 CRC64;
SQ
Query Match 82.2%; Score 545; DB 2; Length 329;
Best Local Similarity 80.3%; Pred. No. 1.7e-44;
Matches 106; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
QY 1 AKLEVTYLGKIGKDGQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 AKLQATLTLSGIRKGGVTLDPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRRNK 61
QY 61 NYKVQYKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBAFVTELAALIASPL 120
DB 62 NYKVQYKIQNPCTSGTCDPSVTRSAVSDFTSFTQYSTVERALVRETELQALLADPM 121
QY 121 LIDAIDQLNPAY 132
DB 122 LVNAIDNLNPAY 133

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded RNA phage Q beta."
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA. Control of A-protein synthesis."
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF052431; AAC06251.1; --
DR HSSP: P03615; 1QBE.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
DR PROSITE: PS00030; RNA_RNP_1; UNKNOWN 1.
DR SEQUENCE 329 AA; 35893 MW; 3E3CD821E625F4 CRC64;
SQ
Query Match 82.2%; Score 545; DB 2; Length 329;
Best Local Similarity 80.3%; Pred. No. 1.7e-44;
Matches 106; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
QY 1 AKLEVTYLGKIGKDGQTLVLPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 2 AKLQATLTLSGIRKGGVTLDPNGVNPPTNGVASTSQAGAVPALERKRVTVSVSOPSRRNK 61
QY 61 NYKVQYKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBAFVTELAALIASPL 120
DB 62 NYKVQYKIQNPCTSGTCDPSVTRSAVSDFTSFTQYSTVERALVRETELQALLADPM 121
QY 121 LIDAIDQLNPAY 132
DB 122 LVNAIDNLNPAY 133
RESULT 9
COAT_BPSP STANDARD; PRT; 132 AA.
ID COAT_BPSP
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A10levivirus.
OC NCB1_TaxID=12027;
RN [1]
RP SEQUENCE FROM N.A.
RA Hiraehima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP."
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL: X07489; CAA0374.1; --
DR HSSP: P03615; 1QBE.

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DR InterPro: IPR002703; Levi_coat.
 DR Pfam: PF01819; Levi_coat; 1.
 KW Coat protein; RNA-binding.
 SQ SEQUENCE 132 AA; 14129 MW; 50B1E6CC6AFOA254 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 132;
 Best Local Similarity 79.5%; Pred. No. 3.2e-44;
 Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLEETVTLGKIGDKQTLVLPNGVNPPTNGVSLSOAGAVPALBKRVTVSQPSRNK 60
 DB 2 AKLNQVTLKIGKNGQTLTLTPRGVNPPTNGVSLSEAGAVPALBKRVTVSQPSRNK 61
 QY 61 NYKVQVKTIONPACTANGSCDPSVTROKYADVTFSTQYSTDERRAFVTELAALASP 120
 DB 62 NFKVQIKONPACTKD-ACDPSVTRSAFADVTLSFTSYSTDERALIRTELAALADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IYDAIDNINPAY 132

RESULT 10
 VAL_BPSP STANDARD; PRT; 331 AA.
 AC P09677;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Readthrough protein A1 [contains: Coat protein].
 OS Bacteriophage SP.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allolevivirus.
 OX NCBI_Taxid=12027;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289362; PubMed=3399390;
 RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
 RT "Analysis of the complete nucleotide sequence of the group IV RNA
 RT coliphage SP.";
 RL Nucleic Acids Res. 16:6205-6221(1988).
 CC -1- FUNCTION: Not yet known.
 CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
 CC protein sequence.

CC -----
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DR EMBL: X07489; CAB37299.1; -.
 DR PIR: S01964; S01964.
 DR HSSP: P03615; 10BE.
 DR InterPro: IPR002703; Levi_coat.
 DR Pfam: PF01819; Levi_coat; 1.
 KW Coat protein.
 FT CHAIN 1 132
 FT CHAIN 1 331
 SQ SEQUENCE 331 AA; 36203 MW; 4A6642E4B52C6582 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 331;
 Best Local Similarity 79.5%; Pred. No. 9.2e-44;
 Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLEETVTLGKIGDKQTLVLPNGVNPPTNGVSLSOAGAVPALBKRVTVSQPSRNK 60
 DB 2 AKLNQVTLKIGKNGQTLTLTPRGVNPPTNGVSLSEAGAVPALBKRVTVSQPSRNK 61
 QY 61 NYKVQVKTIONPACTANGSCDPSVTROKYADVTFSTQYSTDERRAFVTELAALASP 120
 DB 121 IYDAIDNINPAY 132

DB 62 NFKVQIKONPACTKD-ACDPSVTRSAFADVTLSFTSYSTDERALIRTELAALADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IYDAIDNINPAY 132

RESULT 11
 O9TOR8 PRELIMINARY; PRT; 132 AA.
 ID O9TOR8;
 AC O9TOR8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Major coat protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Allolevivirus.
 OX NCBI_Taxid=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RT RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder M.J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF059243; AAC14703.1; -.
 DR HSSP: P03615; 10BE.
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR002703; Levi_coat.
 DR Pfam: PF01819; Levi_coat; 1.
 KW Coat protein.
 SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 75.0%; Score 497.5; DB 2; Length 132;
 Best Local Similarity 75.8%; Pred. No. 2.4e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 AKLEETVTLGKIGDKQTLVLPNGVNPPTNGVSLSOAGAVPALBKRVTVSQPSRNK 60
 DB 2 AKLNQVTLKIGKNGQTLTLTPRGVNPPTNGVSLSEAGAVPALBKRVTVSQPSRNK 61
 QY 61 NYKVQVKTIONPACTANGSCDPSVTROKYADVTFSTQYSTDERRAFVTELAALASP 120
 DB 62 NFKVQIKONPACTKD-ACDPSVTRSSGRDVTLSFTSYSTDERALIRTELAALADPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IYDAIDNINPAY 132

RESULT 12
 O64310 PRELIMINARY; PRT; 330 AA.
 ID O64310;
 AC O64310;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Al-protein.
 OS Enterobacteria phage NL95.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

OC A10Levivirus.
 OX NCBI_TaxID=75725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Post R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; A014704.1; -.
 DR HSP; P03615; 10BE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1 coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Lev1 coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 330 AA; 36175 MW; 961E55F408334410 CRC64;
 Query Match 75.0%; Score 497.5; DB 2; Length 330;
 Best Local Similarity 75.8%; Pred. No. 7.1e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKETVTGKIGKDGKQTLVNPGRVPTNGVSLGAGVPALEKRYTVSVQPSNRK 60
 DB 2 AKNKVTLTGKGNQTLTLPRGVNPTNGVSLGAGVPALEKRYTVSVQPSNRK 61
 QY 61 NYKQVQIOMPACTANGSCDPSVTRQKVDVTFSPQYSTDEERAFVTELAALASPL 120
 DB 62 NYKQVQIOMPACTANGSCDPSVTRQKVDVTFSPQYSTDEERAFVTELAALASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 IVDADINLNPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR STANDARD; PRT; 131 AA.
 AC P03615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OX NCBI_TaxID=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhasee P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1.";
 RL Eur. J. Biochem. 94:375-386(1979).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR InterPro; IPR002703; Lev1 coat.
 DR Pfam; PF01819; Lev1 coat; 1.
 KW Coat protein; direct protein sequencing; RNA-binding;
 SQ SEQUENCE 131 AA; 14535 MW; E7E639E150FC612 CRC64;

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0027;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTLVNPGRVPTNGVSLGAGVPALEKRYTVSVQPSNRKRYKVQV 66
 DB 4 QNLVLDREATPNDRTPVPRDIRDVNGEVSTGVPIESRPTISLRITSNGR--YKSTL 61
 QY 67 KIQNP--ACTANGSCDPSVTRQKVDVTFSPQYSTDEERAFVTELAALASPL 122
 DB 62 KIIVPVQSGQIVNGVTVPVVATSVTYVDYDASTTKERNFVGMTADALKADLMVH 121
 QY 123 DAIDQINPAY 132
 DB 122 DTLVNLQGVY 131
 RESULT 14
 ID Q8VDC2 PRELIMINARY; PRT; 473 AA.
 AC Q8VDC2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Tmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kiss H., Darat E., Kiss C., Kost-Alimova M., Klein G., Dumaneki J.P.,
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3.";
 RL Mamm. Genome 13:646-655(2002).
 DR EMBL; AJ248064; CAD20986.1; -.
 DR MGD; MGI:2446841; Tmem7.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0E69F2A4D CRC64;
 Query Match 14.0%; Score 93; DB 2; Length 473;
 Best Local Similarity 26.1%; Pred. No. 2;
 Matches 40; Conservative 17; Mismatches 34; Indels 62; Gaps 6;
 QY 22 NPERGVNPTNG--VASLSQAGAVP-----ALEKRYTVSVQPSNRKRYKVQV---- 66
 DB 219 NPOASNPTRKNDPVSCTSKPAPPLSPSTLSKARBEKVTVTCSNISRSSSSKVPQOAS 278
 QY 67 ----KIQNP-----ACTANGSCDPSVTRQ-----KY 89
 DB 279 KNPQTSNPTRKNDPVSCTSKPAPPLSPSTLSKARBEKVTVTCSNISRSSSSKVPQOAS 338
 QY 90 ADVTFSTQYSTDEERAFVTELAALASPL 122
 DB 339 ADVAKENTRSKTPK-----ALLSSPLVY 361
 RESULT 15
 ID TACY_LISSE STANDARD; PRT; 530 AA.
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligeriolysin precursor (Thiol-activated cytolysin).
 GN Name=Isol;
 OS Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.

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OM protein - protein search, using sw model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-6

Perfect score: 664
Sequence: 1 ALEFVTLGNIGRDGKQTLV.....AALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp19808:***
2: geneseqp19908:***
3: geneseqp20008:***
4: geneseqp20018:***
5: geneseqp20028:***
6: geneseqp20038:***
7: geneseqp20048:***
8: geneseqp20058:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	664	100.0	132 5	ABG94316
2	664	100.0	132 5	ABG80628 Bacteriop
3	664	100.0	132 6	ABR56452 Bacteriop
4	664	100.0	132 6	ABU09689 Bacteriop
5	664	100.0	132 6	ABR44555 Bacteriop
6	664	100.0	132 7	ADD24130 Bacteriop
7	664	100.0	132 7	ADJ82056 Protein f
8	664	100.0	132 7	ADK17144 Virus-lik
9	664	100.0	132 8	ADJ36313 Bacteriop
10	664	100.0	132 8	ADJ67159 Phage Qbe
11	664	100.0	132 8	ADK52193 Bacteriop
12	661	99.5	132 5	ABG94318
13	661	99.5	132 5	ABG80630 Bacteriop
14	661	99.5	132 6	ABR56454 Bacteriop
15	661	99.5	132 6	ABU09691 Bacteriop
16	661	99.5	132 6	ABR44557 Bacteriop
17	661	99.5	132 7	ADD24132 Bacteriop
18	661	99.5	132 7	ADJ82058 Protein f
19	661	99.5	132 7	ADK17146 Virus-lik
20	661	99.5	132 8	ADJ36315 Bacteriop
21	661	99.5	132 8	ADJ67161 Phage Qbe
22	661	99.5	132 8	ADK52195 Bacteriop
23	658	99.1	132 5	ABG94320
24	658	99.1	132 5	ABG80632 Bacteriop
25	658	99.1	132 6	ABR56455 Bacteriop

26	658	99.1	132 6	ABU09693 Bacteriop
27	658	99.1	132 6	ABR44558 Bacteriop
28	658	99.1	132 7	ADD24133 Bacteriop
29	658	99.1	132 7	ADJ82059 Protein f
30	658	99.1	132 7	ADK17147 Virus-lik
31	658	99.1	132 8	ADJ36316 Bacteriop
32	658	99.1	132 8	ADJ67162 Phage Qbe
33	658	99.1	132 8	ADK52196 Bacteriop
34	655	98.6	132 5	ABG94233 Bacteriop
35	655	98.6	132 5	ABG94317
36	655	98.6	132 5	ABG94319
37	655	98.6	132 5	ABG80629 Bacteriop
38	655	98.6	132 5	ABG80631 Bacteriop
39	655	98.6	132 5	ABG80545 Bacteriop
40	655	98.6	132 5	ABR56456 Bacteriop
41	655	98.6	132 6	ABR56439 Bacteriop
42	655	98.6	132 6	ABR56453 Bacteriop
43	655	98.6	132 6	ABU09686 Bacteriop
44	655	98.6	132 6	ABU09690 Bacteriop
45	655	98.6	132 6	ABU09692 Bacteriop

ALIGNMENTS

RESULT 1	ABG94316	ABG94316 standard; protein; 132 AA.
XX	ABG94316;	
XX	29-AUG-2003 (revised)	
DT	10-DEC-2002 (first entry)	
XX		
DE	PQB240 protein.	
XX		
XX	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;	
KW	cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;	
KM	vaccine; infectious disease.	
XX		
OS	unidentified bacteriophage.	
XX		
PN	W0200256905-A2.	
XX		
PD	25-JUL-2002.	
XX		
PF	21-JAN-2002; 2002WC-IB000166.	
XX		
PR	19-JAN-2001; 2001US-0262379P.	
PR	04-MAY-2001; 2001US-0288549P.	
PR	05-OCT-2001; 2001US-0326988P.	
PR	07-NOV-2001; 2001US-0331045P.	
XX		
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
PI	Renner WA, Bachmann M, Tiesot A, Maurer P, Lechner F, Sebbel P;	
PI	Ploesek C;	
XX		
DR	WPI; 2002-627351/67.	
XX		
PT	Molecular antigen array used in the production of vaccines for infectious	
PT	diseases.	
XX		
PS	Claim 18; Page 144; 441pp; English.	
XX		
CC	This invention relates to a novel ordered and repetitive antigen array	
CC	used in the production of vaccines for infectious diseases. The invention	
CC	also discloses a composition comprising a non-natural molecular scaffold	
CC	comprising a core particle selected from a core particle of a non-natural	
CC	origin and a core particle of natural origin and an organiser comprising	
CC	at least one first attachment site, where the organiser is connected to	
CC	the core particle by at least one covalent bond. Also disclosed is an	
CC	antigen or antigenic determinant with at least one second attachment	

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abetal-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.1e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRGKQTLVLRGVNPTNGVASTLSQAGVAPLAEKRVTVSOPSNRK 60
 Db 1 AKLETVTLGNIGRGKQTLVLRGVNPTNGVASTLSQAGVAPLAEKRVTVSOPSNRK 60
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTFYSTDBERAFVRETLAALLASPL 120
 Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTFYSTDBERAFVRETLAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 Db 121 LIDAIDQLNPAY 132

RESULT 2

ABG80628 standard; protein; 132 AA.

AC ABG80628;
 XX 29-NOV-2002 (first entry)

DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-240.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.

OS Synthetic.

XX WO200256907-A2.

XX 25-JUL-2002.

PF 21-JAN-2002; 2002WO-IB000168.

PR 19-JAN-2001; 2001US-0262379P.

PR 04-MAY-2001; 2001US-0286549P.

PR 05-OCT-2001; 2001US-0326989P.

PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVA) NOVARIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEB) LUEBEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.

PI Maurer P, Lechner F, Ortmann R, Luecend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tiesot A, Sebbel P, Plosek C;
 XX WPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

XX Example 18; Page 144; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
 CC or C-terminal linker peptide which serves as the scaffold protein). The
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array

SO Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.1e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRGKQTLVLRGVNPTNGVASTLSQAGVAPLAEKRVTVSOPSNRK 60
 Db 1 AKLETVTLGNIGRGKQTLVLRGVNPTNGVASTLSQAGVAPLAEKRVTVSOPSNRK 60
 QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTFYSTDBERAFVRETLAALLASPL 120
 Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTFYSTDBERAFVRETLAALLASPL 120
 QY 121 LIDAIDQLNPAY 132
 Db 121 LIDAIDQLNPAY 132

RESULT 3

ABR56452 standard; protein; 132 AA.

XX ABR56452;
AC
XX
DT 28-JUL-2003 (first entry)
XX
DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:23.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KM cytotoxic; virucide; antibacterial; antiparasitic; fungicide;
KM antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
KM antihypertensive; antidiabetic; neuroprotective; nootropic; osteopathic;
KM antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KM inflammatory autoimmune disease.
XX
XX Bacteriophage Qbeta.
OS Synthetic.
XX
XX WO2003024480-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 16-SEP-2002; 2002WO-IB004252.
XX
XX PR 14-SEP-2001; 2001US-0318967P.
XX
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M, Storni T, Lechner F;
PI
XX WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX Disclosure; Page 179-180; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytotoxic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
CC antihypertensive, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumors and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60

DB 1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NKVKQVKIONPACTANGSCDPSVTROKAYADVTFSTQSTDEBFAFVTELAALNAPL 120
DB 61 NKVKQVKIONPACTANGSCDPSVTROKAYADVTFSTQSTDEBFAFVTELAALNAPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132
RESULT 4
ABU09689
ID ABU09689 standard; protein; 132 AA.
XX
XX ABU09689;
AC
XX
XX 03-UTL-2003 (first entry)
XX
XX DE Bacteriophage Qbeta mutant coat protein #1.
XX
XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
KM cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KM renin-activated angiotensin system; hypertension; stroke; infarction;
KM congestive heart failure; kidney failure; retinal haemorrhage; mutant;
XX muteln.
XX
XX Bacteriophage Qbeta.
OS
XX WO2003031466-A2.
XX
XX PD 17-APR-2003.
XX
XX PF 07-OCT-2002; 2002WO-EP011219.
XX
XX PR 05-OCT-2001; 2001US-0326998P.
XX
XX PR 07-NOV-2001; 2001US-0331045P.
XX
XX PR 18-JAN-2002; 2002US-00050902.
XX
XX PR 21-JAN-2002; 2002WO-IB000166.
XX
XX PR 19-UTL-2002; 2002US-0396637P.
XX
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M;
PI
XX WPI; 2003-430264/40.
XX
XX DR New angiotensin peptide moiety carrier conjugate comprising a carrier and
XX an angiotensin peptide moiety, useful for treating or preventing a
XX PT disorder associated with renin-activated angiotensin, e.g. hypertension
XX or infarction.
XX
XX PS Claim 20; Page 93-94; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate
CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC mutant bacteriophage Qbeta coat protein used in the preparation of the
CC vaccine conjugates of the invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGKQTLVLRGVNPTNGVASLSQAGVPALEKRVTVSVSOPSRRNK 60
 DB 1 AKLEVTTLGNIGDGGKQTLVLRGVNPTNGVASLSQAGVPALEKRVTVSVSOPSRRNK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120

QY 121 LIDAIQDLNPAY 132
 DB 121 LIDAIQDLNPAY 132

RESULT 5
 ABR44555
 ID ABR44555 standard; protein; 132 AA.

XX ABR44555;
 XX
 DT 25-JUL-2003 (first entry)

XX Bacteriophage Q-beta coat protein mutant SEQ ID NO:23.
 DE
 XX
 XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KM hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KM immunostimulant; cytotoxic; antiallergic; virucide; antibacterial;
 KM immune response; immunisation; allergy; tumour; breast cancer;
 KM neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KM chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX Bacteriophage Qbeta.
 OS
 OS Synthetic.
 XX
 XX WO2003024481-A2.
 XX
 XX 27-MAR-2003.
 PD
 XX
 XX 16-SEP-2002; 2002WO-IB004132.
 PF
 XX
 XX 14-SEP-2001; 2001US-0318994P.
 PR
 XX 22-APR-2002; 2002US-0374145P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER) MAURER P.
 PA (TISSE) TISSEOT A.
 PA (SCHW) SCHWARZ K.
 PA (MEID) MEIJERINK E.
 PA (LIPPO) LIPOMSKY G.
 PA (PUMP) PUMPENS P.
 PA (CIEL) CIELENS I.
 PA (RENH) RENHOFA R.

XX Maurer P, Tisseot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storm T;
 XX WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.

XX
 XX Disclosure; Page 259; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the vaccine; and
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention

XX
 SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best local Similarity 100.0%; Pred. No. 1.1e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGKQTLVLRGVNPTNGVASLSQAGVPALEKRVTVSVSOPSRRNK 60
 DB 1 AKLEVTTLGNIGDGGKQTLVLRGVNPTNGVASLSQAGVPALEKRVTVSVSOPSRRNK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120
 DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALASPL 120

QY 121 LIDAIQDLNPAY 132
 DB 121 LIDAIQDLNPAY 132

RESULT 6
 ADD24130
 ID ADD24130 standard; protein; 132 AA.

XX ADD24130;
 AC
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX
 XX Bacteriophage Qbeta coat protein mutant Qbeta-240.
 DE
 XX
 XX vaccine composition; virus-like particle; core particle;
 KM first attachment site; antigen; antigenic determinant; prion protein;
 KM PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KM prion disease; Bovine Spongiform Encephalopathy; BSE;
 KM Creutzfeldt-Jakob Disease; coat protein; mutant; mutein.

XX
 OS
 OS Synthetic.
 OS Bacteriophage Qbeta.
 XX
 XX WO2003059386-A2.
 XX
 XX 24-JUL-2003.
 PD
 XX
 XX 17-JAN-2003; 2003WO-EP000460.
 PF
 XX
 XX 18-JAN-2002; 2002US-00050902.
 PR
 XX 21-JAN-2002; 2002WO-IB000166.
 PR
 XX 08-JUL-2002; 2002US-0393725P.
 PR
 XX 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX
 XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 PI WPI; 2003-598483/56.
 XX
 XX A vaccine composition for preventing or treating prion diseases (e.g.

PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

Example 1; SEQ ID NO 23; 246pp; English.

CC This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (PrP) or its dimer, or a PrP peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is the amino acid sequence of a mutant coat protein from bacteriophage Obera which may be used during the creation of the vaccine composition of the invention.

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
DB 1 AKLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NKKVQVKIONPPTACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
DB 61 NKKVQVKIONPPTACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 7
ADJ82056
ID ADJ82056 standard; protein; 132 AA.

AC ADJ82056;
DT 06-MAY-2004 (first entry)

DE Protein for RANKL antigen array to treat bone disease.

KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
KW bone disease; encephalopathy; immune system stimulation.

OS Unidentified.

PN WO2003039225-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012449.

PR 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Maurer P, Spohn G;

DR WPI; 2003-44130/41.

PT New compositions comprising a core particle and at least one antigen or antigenic determinant, useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies.

XX Disclosure; SEQ ID NO 23; 222pp; English.

CC The invention relates to a composition comprising a core particle having at least one first attachment site, and at least one antigen or antigenic determinant having at least one second attachment site. The antigen or antigenic determinant is a RANKL protein, RANKL fragment or RANKL peptide. The second attachment site is (non-) naturally occurring with the antigen or antigenic determinant, and is capable of association to the first attachment site. The antigen or antigenic determinant and the core particle interact through the association to form an ordered and repetitive antigen array. The composition is useful as a medicament, or for the manufacture of a medicament for treating bone diseases. The composition is especially useful for as a vaccine for therapy or prophylaxis of bone diseases, particularly mammalian encephalopathies, and for stimulating mammalian immune system. This sequence represents a protein of the invention.

CC Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
DB 1 AKLEVTTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NKKVQVKIONPPTACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
DB 61 NKKVQVKIONPPTACTANGSCDPSVTRQKADVTFSFTQSTDEERAFVTELAALLASPL 120
QY 121 LIDAIIDQINPAY 132
DB 121 LIDAIIDQINPAY 132

RESULT 8
ADK17144
ID ADK17144 standard; peptide; 132 AA.

AC ADK17144;

DT 06-MAY-2004 (first entry)

DE Virus-like particle repetitive antigen array peptide #23.

KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;
KW interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

OS Unidentified.

PN WO2003040164-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012455.

PR 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Jennings G, Sonderegger I;

DR WPI; 2003-441518/41.

PT Composition comprising an ordered and repetitive antigen or antigenic determinant array, useful as a medicament, or for manufacturing a medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's Lymphoma.
XX
PS Disclosure; SEQ ID NO 23; 245pp; English.
XX
CC The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC compositions are useful as medicaments; or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFVTELAALIASPL 120
QY 121 LIDAIIDQINPAY 132
Db 121 LIDAIIDQINPAY 132
RESULT 9
ADJ36313
ID ADJ36313 standard; protein; 132 AA.
XX
AC ADJ36313;
XX
DT 22-APR-2004 (first entry)
XX
DE Bacteriophage AP205 coat protein virus-like particle.
XX
KM antiallergic; cytostatic; virucide; immunostimulant; vaccine;
KM immune response; virus-like particle; immunostimulatory; allergy; tumour;
KM chronic disease; chronic viral disease; RNA bacteriophage; coat protein;
KM VLP; adjuvant.
XX
OS Bacteriophage AP205.
XX
PN WO200400351-A1.
XX
PD 31-DEC-2003.
XX
PP 20-JUN-2003; 2003WO-EP006541.
XX
PR 20-JUN-2002; 2002US-0389898P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Renner WA;
XX
DR WPI; 2004-108361/11.
XX
PT New compositions comprising a virus-like particle (VLP), an
PT immunostimulatory substance bound to the VLP, and an antigen mixed with
PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.
XX
PS Disclosure; SEQ ID NO 14; 252pp; English.
XX
CC The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC disease such as allergies, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of an RNA bacteriophage
CC coat protein a virus like particle (VLP) that can be used in the adjuvant
CC of the invention.
XX
SQ Sequence 132 AA;
Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
Db 1 AKLEVTTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFVTELAALIASPL 120
Db 61 NYKVQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBERAFVTELAALIASPL 120
QY 121 LIDAIIDQINPAY 132
Db 121 LIDAIIDQINPAY 132
RESULT 10
ADJ67159
ID ADJ67159 standard; protein; 132 AA.
XX
AC ADJ67159;
XX
DT 06-MAY-2004 (first entry)
XX
DE Phage Qbeta coat protein mutant Qbeta 240 for antigen display array.
XX
KM anorectic; core particle; antigenic determinant; ghrelin; P-pillin;
KM antigenic array.
XX
OS Bacteriophage Qbeta.
OS Synthetic.
XX
PN WO2004009124-A2.
XX
PD 29-JAN-2004.
XX
PF 18-JUL-2003; 2003WO-EP007849.
XX
PR 19-JUL-2002; 2002US-0396638P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann MF, Fulurija A;
XX
DR WPI; 2004-132866/13.
XX
PT New composition comprising a core particle having a first attachment site
PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
PT peptide having a second attachment site, useful for treating obesity.
XX
PS Disclosure; SEQ ID NO 17; 175pp; English.
XX
CC The invention relates to a new composition comprising: (i) a core
CC particle with at least one first attachment site; and (ii) at least one
CC antigen or antigenic determinant with at least one second attachment

XX Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 XX
 PS Claim 18; Page 145; 441pp; English.
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, anti-allergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)
 XX
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 2,4e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLETTTLGNIGDGGKOTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
 DB 1 ARLETTTLGNIGDGGKOTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
 QY 61 NYKVOVKIQNPACTANGSCDPSVTRQKADVTFPSFTQVSTDEBRAPVETELAAALSPL 120
 DB 61 NYKVOVKIQNPACTANGSCDPSVTRQKADVTFPSFTQVSTDEBRAPVETELAAALSPL 120
 QY 121 LIDAIIDQLNPNAY 132
 DB 121 LIDAIIDQLNPNAY 132
 RESULT 13
 ABG80630 standard; protein; 132 AA.
 XX
 XX ABG80630;
 XX 29-NOV-2002 (first entry)
 XX Bacteriophage Q-beta A1 coat protein mutant Qbeta-250.
 DE Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 XX
 PN MO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 XX 21-JAN-2002; 2002MO-IB000168.
 PF 19-JAN-2001; 2001US-0262379P.
 XX 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326598P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUBO/) LUBOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 XX Maurer P, Lechner F, Ortmann R, Lucend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Flosek C;
 XX
 XX WPI; 2002-636514/68.
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 XX
 PS Example 18; Page 145; 418pp; English.
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 2,4e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKLETTTLGNIGDGGKOTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60
 1 ARLETTTLGNIGDGGKOTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSQPSRNRK 60

DB 1 ARLEVTTLGNIRGDKQTLVLNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
 QY 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSTQYSTDBERAFVTELAALLASPL 120
 DB 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSTQYSTDBERAFVTELAALLASPL 120
 QY 121 LIDAIDQOLNPAY 132
 DB 121 LIDAIDQOLNPAY 132
 RESULT 14
 ABR56454
 ID ABR56454 standard; protein; 132 AA.
 AC ABR56454;
 XX
 DT 28-JUL-2003 (first entry)
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO.25.
 XX
 KW Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytosolic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
 KW antihydrolytic; antidiabetic; neuroprotective; nocotropic; osteopathic;
 KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 OS
 XX WO2003024480-A2.
 PN
 PD 27-MAR-2003.
 XX
 PF 16-SEP-2002; 2002WO-IB004252.
 XX
 PR 14-SEP-2001; 2001US-0318967P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann MF, Storni T, Lechner F;
 XX
 DR WPI; 2003-363095/34.
 XX
 PT A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX
 PS Disclosure; Page 181; 243pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen. or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antidiabetic, antinflammatory,
 CC antihydrolytic, antirheumatic, neuroprotective, nocotropic, osteopathic,
 CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumors and infectious diseases such as viral, bacterial,

CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 6; Length 132;
 Best Local Similarity 99.2%; Pred. No. 2.4e-70;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLEVTTLGNIRGDKQTLVLNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
 DB 1 ARLEVTTLGNIRGDKQTLVLNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
 QY 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSTQYSTDBERAFVTELAALLASPL 120
 DB 61 NTKVQVKIONPTACTANGSCDPSVTRQKYADVTFSTQYSTDBERAFVTELAALLASPL 120
 QY 121 LIDAIDQOLNPAY 132
 DB 121 LIDAIDQOLNPAY 132
 RESULT 15
 ABU09691
 ID ABU09691 standard; protein; 132 AA.
 XX
 AC ABU09691;
 XX
 DT 03-JUL-2003 (first entry)
 XX
 DE Bacteriophage Qbeta mutant coat protein #3.
 XX
 KW Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW
 XX
 OS Bacteriophage Qbeta.
 XX
 PN WO2003031466-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 07-OCT-2002; 2002WO-BP011219.
 XX
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann M;
 XX
 DR WPI; 2003-430264/40.
 XX
 PT New angiotensin peptide moiety carrier conjugate comprising a carrier and
 PT an angiotensin peptide moiety, useful for treating or preventing a
 PT disorder associated with renin-activated angiotensin, e.g. hypertension
 PT or infarction.
 XX
 PS Claim 20; Page 94; 97pp; English.
 XX
 CC The invention describes an angiotensin peptide moiety carrier conjugate
 CC comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second

CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC mutant bacteriophage ϕ beta coat protein used in the preparation of the
CC vaccine conjugates of the invention
XX
SQ Sequence 132 AA;

SQ Sequence 132 AA;

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Best Local Similarity	99.2%	Pred	No	2.4e-70			
Matches	131	Conservative	1	Mismatches	0	Indels	0
						Gaps	0

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Db	1	ARLETTVLGNIGDGGKQTLVLNPRGVNPTNGVASLSQAGVPALEKRYTVSVSPSNRK	60
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Db	61	NYKQVQVIQNPCTCTANGSCDPSVTRQKADVTFSTQYSTDDEERAFTRELAALLSPL	120
QY	121	LIDAIDQNLNPAV	132
	:	:	:
Db	121	LIDAIDQNLNPAV	132

Search completed: January 4, 2005, 09:11:00
Job time : 40.6824 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:05:21 ; Search time 10.3622 Seconds
(without alignments)
844,801 Million cell updates/sec

Title: US-10-622-064-6

Perfect score: 664

Sequence: 1 AALEVTYGNIGRDKQITV.....AALLSPILIDALDLPAY 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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9: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.5	12.3	626	4	US-09-485-717-2
2	81.5	12.3	626	4	US-09-948-722-2
3	75	11.3	409	4	US-09-328-352-4249
4	71.5	10.8	916	4	US-09-252-991A-23637
5	70.5	10.6	502	4	US-09-270-767-44620
6	69.5	10.5	129	1	US-08-090-148-1
7	69	10.4	300	4	US-09-302-626B-182
8	69	10.4	622	4	US-09-302-626B-185
9	69	10.4	766	4	US-09-538-092-216
10	69	10.4	1073	4	US-09-206-942-47
11	69	10.3	1079	4	US-09-206-942-47
12	68.5	10.3	381	4	US-09-198-452A-745
13	68.5	10.3	383	3	US-09-045-186-2
14	68.5	10.3	384	1	US-08-332-144-4
15	68.5	10.3	384	2	US-08-555-268A-15
16	68.5	10.3	384	3	US-09-200-673-15
17	68.5	10.3	384	4	US-10-013-846-4
18	68.5	10.3	384	5	US-09-708-392-9
19	68.5	10.3	384	5	PCT-US93-05039-3
20	68.5	10.3	411	3	US-08-817-869-3
21	68.5	10.3	411	5	PCT-US95-14377-3
22	68.5	10.3	733	4	US-09-248-796A-16565
23	68.5	10.3	818	4	US-09-252-991A-16691
24	68	10.2	316	4	US-09-270-767-43925
25	68	10.2	316	4	US-09-270-767-59331
26	67.5	10.2	424	3	US-09-173-581-7
27	67.5	10.2	424	3	US-09-420-915-7

28	67.5	10.2	428	3	US-09-134-001C-2885	Sequence 2885, Ap
29	67.5	10.2	1328	3	US-08-781-891-76	Sequence 76, Appl
30	67.5	10.2	1328	4	US-09-618-166-76	Sequence 76, Appl
31	67	10.1	322	4	US-09-328-352-6759	Sequence 6759, Ap
32	67	10.1	632	4	US-09-976-594-41	Sequence 41, Appl
33	66.5	10.0	279	3	US-08-397-411-13	Sequence 13, Appl
34	66.5	10.0	398	6	5495001-9	Patent No. 5495001
35	66.5	10.0	415	4	US-09-252-991A-29602	Sequence 29602, A
36	66.5	10.0	915	4	US-09-206-942-35	Sequence 35, Appl
37	66.5	10.0	1220	4	US-09-206-942-28	Sequence 28, Appl
38	66.5	10.0	1222	4	US-09-206-942-37	Sequence 37, Appl
39	66.5	10.0	1226	4	US-09-206-942-26	Sequence 26, Appl
40	66.5	10.0	1228	4	US-09-206-942-34	Sequence 34, Appl
41	66	9.9	187	3	US-08-916-246-12	Sequence 12, Appl
42	66	9.9	187	3	US-09-949-186-12	Sequence 12, Appl
43	66	9.9	1036	2	US-08-720-484A-5	Sequence 5, Appl
44	66	9.9	1036	3	US-08-953-823A-5	Sequence 5, Appl
45	66	9.9	1036	4	US-09-398-239-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-485-717-2
; Sequence 2, Application US/09485717
; Patent No. 6673353
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan
; APPLICANT: Hesse, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 16862POS
; CURRENT APPLICATION NUMBER: US/09/485,717
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: EP 97114614.7
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/EP98-05109
; PRIOR FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2
Query Match 12.3%; Score 81.5; DB 4; Length 626;
Best Local Similarity 22.0%; Pred. No. 0.3;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;
QY 13 RRGKQITV-----NPRGVNPTNGVASSQGA-----VPALEKRV 48
DB 138 KQGNETIVKKKKKINSQNNADIQVNNALSSITLFGALVKANSELVENQDVLVPRKDSL 197
QY 49 TVSVQSPSHRNKRYQVYQIONPACTANGSCDPSVTR-----QKYADVTFSFTQYSTD 102
DB 198 TISIDLPKGTNDKNTIVK--NATKSNTNNNAVTLVERNKKYAAAYPVS---AKIDVD 252
QY 103 EERAFVTEFLAA 114
DB 253 DEMAYSESQLIA 264
RESULT 2
US-09-948-722-2
; Sequence 2, Application US/09948722
; Patent No. 6776993
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Stefan H. E.
; APPLICANT: Hesse, Jürgen
; TITLE OF INVENTION: Tuberculosis Vaccine

FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
OTHER INFORMATION: escape domain
US-09-948-722-2

Query Match 12.3%; Score 81.5; DB 4; Length 626;
Best Local Similarity 22.0%; Pred. No. 0.3;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;

QY 13 RDGKQTLVL-----NPGVNPPTNGVASLSQAGV-----VPALAEKRV 48
DB 138 KDGNEIVIVEKKKKKSNQNNADIQVNAISLTPGLVYANGSELVENQPDVLPVRKDSL 197
QY 49 TVSVSOPSRNRKRYKQVQKIQNPACTANGSCDPSVTR-----QKADYTFSTQYSTD 102
DB 198 TLEIDLEPGMTQNDKIVVK--NATKSNVNNAVNVLVERMNEKYAQAAPNVS---AKIDYD 252
QY 103 EERAFVRETELA 114
DB 253 DEMAYSESQULA 264

RESULT 3
US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match 11.3%; Score 75; DB 4; Length 409;
Best Local Similarity 25.2%; Pred. No. 1;
Matches 31; Conservative 19; Mismatches 51; Indels 22; Gaps 5;

QY 13 RDGKQTLVLNPR-----GVNPPTNGVASLSQAGVPALEKRVTV-SVSOPSRNRKRYKQ 65
DB 118 RGGRLVNVNPRNALLSFAPVVDGTPPI-----IAKPNQRLITRDLAIGRTGSGN---A 169
QY 66 VKQNPACTANGSCDPSVTRQKADYTFSTQYSTDEERAFVRETELAALLASPLIDAI 125
DB 170 IAVIREGTNNALVDENTAKPYSEITP-----EEVMSYKTIAMLMKASKQIIDL 222
QY 126 DQL 128
DB 223 POL 225

RESULT 4
US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637

Query Match 10.8%; Score 71.5; DB 4; Length 916;
Best Local Similarity 22.9%; Pred. No. 10;
Matches 27; Conservative 17; Mismatches 53; Indels 21; Gaps 4;

QY 9 GNIGRDG-----KQTLVNPGRVNPPTNGVASLSQAGVPALEKRVTVSVS-----OP 55
DB 789 GLIGSGALRLRAALVQARRIDPFGGLAALPVQGLFALQABDFAGGSLDQKRWQA 848
QY 56 SRNRKRYKQVQKIQNPACTANGSCDPSVTRQKADYTFSTQYSTDEERAFVRETE 110
DB 849 EERGAERYAQSNAHREHPCRSIEANADCPISADAGRW-----PWTFSDSATRMALRT 901

RESULT 5
US-09-270-767-44620
Sequence 44620, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44620
LENGTH: 502
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44620

Query Match 10.6%; Score 70.5; DB 4; Length 502;
Best Local Similarity 24.2%; Pred. No. 5.4;
Matches 29; Conservative 20; Mismatches 52; Indels 19; Gaps 4;

QY 18 TLVLANRGVNPPTNGVASLSQAGVPALEKRVTVSVSOP-----SRNRKRYKQVQKIQN 70
DB 258 TLAVN---TSPSPPTPOPIVEPEQEVNSVTVVASPEVPVAVKARNDRKQRTSTIKN 314
QY 71 PFACTANGSCDPSVTRQKADYTFSTQ-----YSTDEERAFVRETELAALLASPL 121
DB 315 AKXVAVTFPCTSSATHTSTRCTISYVSGSLGSPPLGXADKDFVTTLAKPLATFISSPNL 374

RESULT 6
US-08-090-148-1
Sequence 1, Application US/08090148
Patent No. 5534257
GENERAL INFORMATION:

APPLICANT: Maestico, Robert Allan
APPLICANT: Stockley, Peter George
APPLICANT: Talbot, Simon John
TITLE OF INVENTION: Antigen-Presenting Capsid with
TITLE OF INVENTION: Fusion MS2-Coat Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rosenman & Colin
STREET: 575 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10022-2585
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44Mb
COMPUTER: IBM PS2-486
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,148
FILING DATE: 08/11/93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9101550.3
FILING DATE: 01/24/91
APPLICATION NUMBER: PCT/GB92/00124
FILING DATE: 01/22/92
ATTORNEY/AGENT INFORMATION:
NAME: Nissendaum, Israel
REGISTRATION NUMBER: 27,582
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-8636
TELEFAX: (212) 940-6404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: NOT RELEVANT
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: VIRUS
FEATURE:
NAME/KEY: Coat protein from MS2-RNA
NAME/KEY: bacteriophage
LOCATION: Location 1 through 129 below
LOCATION: represents entire MS2 coat
LOCATION: protein in the published
LOCATION: sequence.
PUBLICATION INFORMATION:
AUTHORS: Min Jou, W.; Haegeman, G.;
AUTHORS: Yeebaert, M.; Piers, W.
TITLE: Nucleotide sequence of the
TITLE: gene coding for the
TITLE: bacteriophage MS2 coat protein
JOURNAL: Nature
VOLUME: 237
PAGES: 82-88
DATE: 1972
US-08-090-148-1

Query Match 10.5%; Score 69.5; DB 1; Length 129;
Best Local Similarity 25.0%; Pred. No. 0.85; Mismatches 24; Conservative 16; Mismatches 43; Indels 13; Gaps 2;

QY 27 NPTNGVA-----SLQGAVPALKEKTVSVSQPSNRKRYKQYKIQNPACTANGSC 80
DB 24 NPANGVAMWISSNRSGA-----YKVCVSRRGSSAQNKRYTKIVEPVKATQTVGVGE 76
QY 81 DPSTVRKQKADVTFTSTQYSTDERAFVTEIALLL 116
DB 77 LPVAAMRSYINMBELTIPFATINSCELIIVAMOGLL 112

RESULT 7
US-09-302-626B-182
Sequence 182, Application US/09302626B
Patent No. 6709660
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Massignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 182
LENGTH: 300
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pepa
US-09-302-626B-182

Query Match 10.4%; Score 69; DB 4; Length 300;
Best Local Similarity 23.2%; Pred. No. 3.7; Mismatches 38; Conservative 17; Mismatches 51; Indels 58; Gaps 7;

QY 10 NIGRDKQTLVILNPGVNPFTNGVASLSQAGAV-----PALERKRYT 49
DB 5 NVHRDGSQMDSEASAVRT-GAASVSABAARGFMAAFSVLALGVAAFSAPASGII 63
QY 50 VSVSOPSRNR-----KNTKVQYKIQNPACTANGSCDPSVTRQKADVTFTSTQYSTDR 103
DB 64 ADKSAEPKNOQAVILQTPANGLPQVNIQTPS-----SQGVSVNR-----FKQFQVDR 108
QY 104 E-----RAFVTRTEIALLL-----ASPLIDAIQOLNPA 131
DB 109 KGVILNRSRNTQTQLGWITQGNPHLARGEARVIVQIDSSNPS 152

RESULT 8
US-09-302-626B-185
Sequence 185, Application US/09302626B
Patent No. 6709660
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Massignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 185
LENGTH: 622
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pepa
US-09-302-626B-185

Query Match 10.4%; Score 69; DB 4; Length 622;
Best Local Similarity 23.2%; Pred. No. 12; Mismatches 38; Conservative 17; Mismatches 51; Indels 58; Gaps 7;

QY 10 NIGRDKQTLVLPNGVPTNGVASLSQAGAV-----PALEKRYTV 49
 DB 23 NVHBDGSMODSEASAVTVT-GAASVSABAPAFGRMAASVWALAGVAFAFAPASGIT 81
 QY 50 VSVSOPSRNR-----KRYKQVQKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDE 103
 DB 82 ADSAPKNGQAVLITQANGLPQVNIQTPS-----SQGVSVNR-----FKQFDVDE 126
 QY 104 E-----RAFVTELAAL-----ASPLIIDAIQDLNPA 131
 DB 127 KGVILNNSRSNTQTLGGWITQGNPHLARGEARVYVNIQDISNPS 170

RESULT 9
 US-09-538-092-216
 ; Sequence 216, Application US/09538092
 ; Patent No. 6753314
 ; GENERAL INFORMATION:
 ; APPLICANT: Glot, Loic
 ; APPLICANT: Mansfield, Tracy A.
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 ; FILE REFERENCE: 15966-542
 ; CURRENT APPLICATION NUMBER: US/09/538, 092
 ; CURRENT FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 60/178,965
 ; PRIOR FILING DATE: 2000-02-01
 ; NUMBER OF SEQ ID NOS: 1387
 ; SOFTWARE: CurabatsSeqFormatter Version 0.9
 ; SEQ ID NO 216
 ; LENGTH: 766
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (0)...(0)
 ; OTHER INFORMATION: Polypeptide Accession Number YDR490C
 US-09-538-092-216

Query Match 10.4%; Score 69; DB 4; Length 766;
 Best Local Similarity 23.8%; Pred. No. 16;
 Matches 36; Conservative 25; Mismatches 60; Indels 30; Gaps 7;

QY 5 TVTTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAV-----PALEKRYTVSVS 53
 DB 431 TVKXANIQLAGNGHADPPLQAPATSOHSHVISTMTAATFAFNKDYTSQPKLGSKSTSVR 490
 QY 54 QPSHRKRYKQVQKIQNPACTANGSCDPSVT-----ROKXADVTFSFTQYSTDEER 105
 DB 491 SASNNTREVIQKVSNNRASVSS-----PSISTSRGKDNRSRSDAFWMSRYLQNMN-ER 545
 QY 106 AFVTELAAL-----LASEPLIID-ALDQANP 130
 DB 546 VLLMKVEALSTRNLEDSFVGLHENVALDYKNP 576

RESULT 10
 US-09-206-942-49
 ; Sequence 49, Application US/09206942
 ; Patent No. 6432669
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
 ; FILE REFERENCE: 1038-861 MIS:jb
 ; CURRENT APPLICATION NUMBER: US/09/206,942
 ; CURRENT FILING DATE: 1998-12-08
 ; EARLIER APPLICATION NUMBER: 09/167,568
 ; EARLIER FILING DATE: 1998-10-07

; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 49
 ; LENGTH: 1073
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 US-09-206-942-49

Query Match 10.4%; Score 69; DB 4; Length 1073;
 Best Local Similarity 22.0%; Pred. No. 28;
 Matches 27; Conservative 26; Mismatches 52; Indels 18; Gaps 4;

QY 4 ETVTLNIGRDKQTLVLPNG-----VNPNGVASLSQAGAVPALEKRYTVSVSQ 54
 DB 766 KTLTVGNV--SGWTVVTANRGALTLTAGSTINGTVTSSQSGEIGEVTKTVSVTA 823
 QY 55 PSRN--RKNYKQVQKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVTE 111
 DB 824 TAGSLTVKGAKINATEGATVTLTASSG---KLTTEASSNITSAKQVDLSAQDGSIAQ 879
 QY 112 LAA 114
 DB 880 ISA 882

RESULT 11
 US-09-206-942-47
 ; Sequence 47, Application US/09206942
 ; Patent No. 6432669
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; APPLICANT: Yang, Yan-Ping
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
 ; FILE REFERENCE: 1038-861 MIS:jb
 ; CURRENT APPLICATION NUMBER: US/09/206,942
 ; CURRENT FILING DATE: 1998-12-08
 ; EARLIER APPLICATION NUMBER: 09/167,568
 ; EARLIER FILING DATE: 1998-10-07
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 1079
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 US-09-206-942-47

Query Match 10.4%; Score 69; DB 4; Length 1079;
 Best Local Similarity 22.0%; Pred. No. 28;
 Matches 27; Conservative 26; Mismatches 52; Indels 18; Gaps 4;

QY 4 ETVTLNIGRDKQTLVLPNG-----VNPNGVASLSQAGAVPALEKRYTVSVSQ 54
 DB 772 KTLTVGNV--SGWTVVTANRGALTLTAGSTINGTVTSSQSGEIGEVTKTVSVTA 829
 QY 55 PSRN--RKNYKQVQKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEERAFVTE 111
 DB 830 TAGSLTVKGAKINATEGATVTLTASSG---KLTTEASSNITSAKQVDLSAQDGSIAQ 885
 QY 112 LAA 114
 DB 886 ISA 888

RESULT 12
 US-09-198-452A-745
 ; Sequence 745, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; thereof and uses thereof, in particular for the diagnosis, prevention


```

APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YV/PANCREATIC POLYPEPTIDE
TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,268A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44743-Z/JPM/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-555-268A-15

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Query Match 10.3%; Score 68.5; DB 2; Length 384;
Best Local Similarity 25.0%; Pred. No. 6.4;
Matches 27; Conservative 12; Mismatches 34; Indels 35; Gaps 4;

QY 16 KQTLVNPGRGVNPTN-----GVA---SISQAGAVPALEKRVTVSVSOPSRRKRYKVQVK 67
DB 138 RHQLINRGRPNRRHAYVIGAIWVLAVASSLPFLIQ--VMTDEPFQN----- 186
QY 68 IONPTACTANGSCDPSVTROKRVADVTFSFTQYSTDEERAFVTELAAL 115
DB 187 -----VTLDAYKDKYVCFDQPSDSHRLSYTLLVL 218

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Job time : 11.3622 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-6

Perfect score: 664
Sequence: 1 AKLEVTTLGNIGRDKQTLV.....AALLASPLLDALDQINPAY 132Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	664	100.0	132	14	US-10-243-739-23
2	664	100.0	132	14	US-10-244-065-23
3	664	100.0	132	14	US-10-289-454-23
4	664	100.0	132	14	US-10-050-902-255
5	664	100.0	132	14	US-10-050-898-255
6	664	100.0	132	14	US-10-346-190-23
7	664	100.0	132	15	US-10-465-811-14
8	664	100.0	132	15	US-10-289-456-23
9	664	100.0	132	15	US-10-622-064-6
10	664	100.0	132	15	US-10-622-124-17
11	664	100.0	132	16	US-10-622-087-17
12	661	99.5	132	14	US-10-243-739-25
13	661	99.5	132	14	US-10-244-065-25

14	661	99.5	132	14	US-10-289-454-25	Sequence 25, App1
15	661	99.5	132	14	US-10-050-902-257	Sequence 257, App
16	661	99.5	132	14	US-10-050-898-257	Sequence 25, App1
17	661	99.5	132	14	US-10-346-190-25	Sequence 16, App1
18	661	99.5	132	15	US-10-465-811-16	Sequence 25, App1
19	661	99.5	132	15	US-10-289-456-25	Sequence 8, App1
20	661	99.5	132	15	US-10-622-064-8	Sequence 19, App1
21	661	99.5	132	15	US-10-622-124-19	Sequence 19, App1
22	661	99.5	132	16	US-10-622-087-19	Sequence 26, App1
23	658	99.1	132	14	US-10-243-739-26	Sequence 26, App1
24	658	99.1	132	14	US-10-244-065-26	Sequence 26, App1
25	658	99.1	132	14	US-10-289-454-26	Sequence 259, App
26	658	99.1	132	14	US-10-050-902-259	Sequence 259, App
27	658	99.1	132	14	US-10-050-898-259	Sequence 259, App
28	658	99.1	132	14	US-10-346-190-26	Sequence 26, App1
29	658	99.1	132	15	US-10-465-811-17	Sequence 17, App1
30	658	99.1	132	15	US-10-289-456-26	Sequence 26, App1
31	658	99.1	132	15	US-10-622-064-9	Sequence 9, App1
32	658	99.1	132	15	US-10-622-124-20	Sequence 20, App1
33	658	99.1	132	16	US-10-622-087-20	Sequence 20, App1
34	655	98.6	132	14	US-10-243-739-10	Sequence 10, App1
35	655	98.6	132	14	US-10-243-739-24	Sequence 24, App1
36	655	98.6	132	14	US-10-243-739-27	Sequence 27, App1
37	655	98.6	132	14	US-10-244-065-10	Sequence 10, App1
38	655	98.6	132	14	US-10-244-065-24	Sequence 24, App1
39	655	98.6	132	14	US-10-244-065-27	Sequence 27, App1
40	655	98.6	132	14	US-10-289-454-10	Sequence 10, App1
41	655	98.6	132	14	US-10-289-454-24	Sequence 24, App1
42	655	98.6	132	14	US-10-289-454-27	Sequence 27, App1
43	655	98.6	132	14	US-10-050-902-159	Sequence 159, App
44	655	98.6	132	14	US-10-050-902-256	Sequence 256, App
45	655	98.6	132	14	US-10-050-902-258	Sequence 258, App

ALIGNMENTS

RESULT 1
US-10-243-739-23
; Sequence 23, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001 US/10/243, 739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 23
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLGNIGRDKQTLVLPNGVNPNGVSLGSAQGVLPALERKVVYSQPSRNK 60
DB 1 AKLEVTTLGNIGRDKQTLVLPNGVNPNGVSLGSAQGVLPALERKVVYSQPSRNK 60
QY 61 NKVVQKINPACTANGSCDPSVTRQKXADVTFFSTQSTBEERAFVTEALALASPL 120
DB 61 NKVVQKINPACTANGSCDPSVTRQKXADVTFFSTQSTBEERAFVTEALALASPL 120
QY 121 LLDALDQINPAY 132

Db 121 LIDAIDQNPAY 132

RESULT 2
US-10-244-065-23

Sequence 23, Application US/10244065
Publication No. US2003009668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Scorni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tissot, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Clelens, Indulis
APPLICANT: Renhofs, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDKQTLVLPNGVNPNGVSLSQAGAVPALERKVTYVSQPSNRK 60
DB 1 AKLETVTLGNIGRDKQTLVLPNGVNPNGVSLSQAGAVPALERKVTYVSQPSNRK 60
QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSTFYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSTFYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQNPAY 132
DB 121 LIDAIDQNPAY 132

RESULT 3
US-10-289-454-23

Sequence 23, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
PRIOR FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-240
US-10-289-454-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDKQTLVLPNGVNPNGVSLSQAGAVPALERKVTYVSQPSNRK 60
DB 1 AKLETVTLGNIGRDKQTLVLPNGVNPNGVSLSQAGAVPALERKVTYVSQPSNRK 60
QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSTFYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSTFYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQNPAY 132
DB 121 LIDAIDQNPAY 132

RESULT 4

US-10-050-902-255
Sequence 255, Application US/10050902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Sebbel, Peter
APPLICANT: Plosek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0190004
CURRENT APPLICATION NUMBER: US/10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 255
LENGTH: 132
TYPE: PRT
ORGANISM: QB 240
US-10-050-902-255

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDKQTLVLPNGVNPNGVSLSQAGAVPALERKVTYVSQPSNRK 60
DB 1 AKLETVTLGNIGRDKQTLVLPNGVNPNGVSLSQAGAVPALERKVTYVSQPSNRK 60
QY 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSTFYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQVQKIQNPACTANGSCDPSVTRQKXADVTFSTFYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQNPAY 132
DB 121 LIDAIDQNPAY 132

RESULT 5
US-10-050-898-255
; Sequence 255, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisbet, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Ploesek, Christine
; APPLICANT: Ottmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050, 898
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Ob 240
US-10-050-898-255

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTVLGNIGDGGQTLVLRGVPPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 60
DB 1 AKLETTVLGNIGDGGQTLVLRGVPPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 60

QY 61 NYKVQKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAALLASPL 120
DB 61 NYKVQKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAALLASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 6
US-10-346-190-23
; Sequence 23, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Ob 240
US-10-346-190-23

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTVLGNIGDGGQTLVLRGVPPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 60
DB 1 AKLETTVLGNIGDGGQTLVLRGVPPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 60

QY 61 NYKVQKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAALLASPL 120
DB 61 NYKVQKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAALLASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 7
US-10-465-811-14
; Sequence 14, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-465-811-14

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETTVLGNIGDGGQTLVLRGVPPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 60
DB 1 AKLETTVLGNIGDGGQTLVLRGVPPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 60

QY 61 NYKVQKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAALLASPL 120
DB 61 NYKVQKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAALLASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 8
US-10-289-456-23
; Sequence 23, Application US/10289456

Publication No. US2004003211A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 132
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Q-beta 240 mutant
US-10-289-456-23

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK 60
1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK 60
Db 61 NYKVQVKIQNPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
61 NYKVQVKIQNPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
Qy 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 9
US-10-622-064-6
Sequence 6, Application US/10622064
Publication No. US20040059094A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrick F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,575
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 132
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-622-064-6

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK 60
1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK 60

Db 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK 60
Qy 61 NYKVQVKIQNPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
61 NYKVQVKIQNPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
Db 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
Qy 121 LIDAIQOLNPAY 132

RESULT 10
US-10-622-124-17
Sequence 17, Application US/10622124
Publication No. US20040076645A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Fulurija, Alma
TITLE OF INVENTION: Ghrelin-Carrier Conjugates
FILE REFERENCE: 1700.0340001
CURRENT APPLICATION NUMBER: US/10/622,124
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,638
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 17
LENGTH: 132
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-622-124-17

Query Match 100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK 60
1 AKLETVTLGNIGRDKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVSOPSRNK 60
Db 61 NYKVQVKIQNPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
61 NYKVQVKIQNPTACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
Qy 121 LIDAIQOLNPAY 132
121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 11
US-10-622-087-17
Sequence 17, Application US/10622087
Publication No. US20040141964A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tissot, Alain
APPLICANT: Ortman, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Straufenbiel, Matthias
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,639
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/470,432
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin version 3.2
SEQ ID NO 17

LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Qbeta 240 mutant
US-10-622-087-17

Query Match 100.0%; Score 664; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
DB 1 AKLEVTTLGNIGDGGQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
QY 61 NKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETELAAALASPL 120
DB 61 NKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETELAAALASPL 120
QY 121 LIDAIDQNLNPAAY 132
DB 121 LIDAIDQNLNPAAY 132

RESULT 12
US-10-243-739-25
Sequence 25, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243, 739.
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318, 967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-25

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
DB 1 AKLEVTTLGNIGDGGQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
QY 61 NKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETELAAALASPL 120
DB 61 NKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETELAAALASPL 120
QY 121 LIDAIDQNLNPAAY 132
DB 121 LIDAIDQNLNPAAY 132

RESULT 13
US-10-244-065-25
Sequence 25, Application US/10244065
Publication No. US20030099668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tissot, Alain

APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244, 065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374, 145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318, 994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-25

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
DB 1 AKLEVTTLGNIGDGGQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60
QY 61 NKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETELAAALASPL 120
DB 61 NKVQVKIONPTACTANGSCDPSVTRQKADVTFFSTQYSTDERAFVRETELAAALASPL 120
QY 121 LIDAIDQNLNPAAY 132
DB 121 LIDAIDQNLNPAAY 132

RESULT 14
US-10-289-454-25
Sequence 25, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289, 454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396, 636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050, 902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331, 045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-250
US-10-289-454-25

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDGGQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSQPSRNRK 60

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Db      1 ARLEVTIGNIGRDKQTLVLPNGVNPFTNGVASLSQAGAVPALEKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTQYSTDERAFVFTLALIASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTQYSTDERAFVFTLALIASPL 120
QY      121 LIDAIQOLNPAY 132
Db      121 LIDAIQOLNPAY 132
```

RESULT 15

```
US-10-050-902-257
; Sequence 257, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisecot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebhel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.019004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 250
US-10-050-902-257
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Query Match      99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ARLEVTIGNIGRDKQTLVLPNGVNPFTNGVASLSQAGAVPALEKRVTVSVSQPSNRK 60
Db      1 ARLEVTIGNIGRDKQTLVLPNGVNPFTNGVASLSQAGAVPALEKRVTVSVSQPSNRK 60
QY      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTQYSTDERAFVFTLALIASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSTQYSTDERAFVFTLALIASPL 120
QY      121 LIDAIQOLNPAY 132
Db      121 LIDAIQOLNPAY 132
```

Search completed: January 4, 2005, 09:41:21
Job time : 32.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-6
Perfect score: 664
Sequence: 1 AKLEVTTLGNIGRDKQTLV.....ALLASPLLDIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79;+
1: p1r1: +
2: p1r2: +
3: p1r3: +
4: p1r4: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	98.6	132	1	VCBPOB
2	529.5	79.7	331	1	S01964
3	116	17.5	131	1	VCBPR1
4	87.5	13.2	530	2	S22340
5	85.5	12.9	540	2	T00646
6	81.5	12.3	529	2	S24231
7	81.5	12.3	529	2	A43505
8	81.5	12.3	529	2	AC1100
9	81	12.2	830	2	S57537
10	80.5	12.1	1502	1	RGBYH1
11	77.5	11.7	528	2	S22341
12	77	11.6	432	2	T31660
13	76.5	11.5	136	2	C98221
14	76.5	11.5	136	2	AE3065
15	76.5	11.5	1052	2	C64221
16	76	11.4	130	1	A46324
17	76	11.4	282	2	A10186
18	75.5	11.4	1097	2	AD2572
19	75	11.3	130	1	VCBPGA
20	74.5	11.2	130	1	VCBPR
21	74.5	11.2	161	4	TS5480
22	74.5	11.2	458	2	T49114
23	74.5	11.2	1861	2	T13845
24	74	11.1	340	2	S18650
25	74	11.1	340	2	A42008
26	74	11.1	366	2	F70618
27	73.5	11.1	520	1	ACMSD1
28	73.5	11.1	601	2	A55921
29	73.5	11.1	654	2	S69673

30	73.5	11.1	719	2	T39271	conserved hypothe
31	73	11.0	243	1	VHUP1	nucleocapsid prote
32	73	11.0	430	2	G88884	protein K09B11.10
33	72.5	10.9	129	1	VCBPR2	coat protein - pha
34	72.5	10.9	129	1	VCBPR7	coat protein - pha
35	72.5	10.9	129	1	VCBPR2	coat protein - pha
36	72.5	10.9	289	2	C70400	ferredoxin oxidore
37	72	10.8	248	2	A86786	conserved hypothe
38	72	10.8	1461	2	E90696	hypochemical prote
39	72	10.8	1461	2	A85547	hypochemical prote
40	71.5	10.8	640	2	S48423	hypochemical prote
41	71	10.7	376	2	C84316	hypochemical prote
42	71	10.7	399	1	A43685	polymerase-associa
43	71	10.7	463	2	S00676	translational elonga
44	70.5	10.6	191	2	H90078	hypochemical prote
45	70	10.5	1545	2	T42751	sulfonylurea recep

ALIGNMENTS

RESULT 1
VCBPOB
coat protein - phage Q-beta
C:Species: phage Q-beta
C:Date: 29-Jul-1981 #sequence.revision 24-Sep-1981 #text_change 09-Jul-2004
C:Accession: A92240; A92221; A92088; A04224
R:Scamir, C.; Sasser, P.A.; Billeter, M.A.
J. Biol. Chem. 253, 8390-8399, 1978
A:Title: Determination of the first half of the coat protein cistron of bacteriophage Qb
A:Reference number: A92240; PMID:79048469; PMID:361741
A:Accession: A92240
A:Molecule type: mRNA
A:Residues: 1-80 <ESD>
A:Cross-references: UNIPROT:P03615
R:Stoll, E.; Wilson, K.J.; Reiser, J.; Weisemann, C.
J. Biol. Chem. 252, 990-993, 1977
A:Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.
A:Reference number: A92221; PMID:77118576; PMID:838709
A:Accession: A92221
A:Molecule type: protein
A:Residues: 1-60 <STO>
R:Malta, T.; Konigsberg, W.
J. Biol. Chem. 246, 5003-5024, 1971
A:Title: The amino acid sequence of the Qbeta coat protein.
A:Reference number: A92088; PMID:71288580; PMID:5570434
A:Accession: A92088
A:Molecule type: protein
A:Residues: 1-21, 'D', '23-55, 57-132 <MAI>
C:Superfamily: phage GA coat protein

Query Match 98.6%; Score 655; DB 1; Length 132;
Best Local Similarity 98.5%; Pred. No. 2.6e-57;
Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	AKLEVTTLGNIGRDKQTLV	NPRTGVSLSQAGVPALEKRVTSVSPSHNRK	60
DB	1	AKLEVTTLGNIGRDKQTLV	NPRTGVSLSQAGVPALEKRVTSVSPSHNRK	60
QY	61	NYKQVYKIQNPACTANGS	CDPSVTROKADVTFSFTYSTDEERAFVRELAALLASPL	120
DB	61	NYKQVYKIQNPACTANGS	CDPSVTROKADVTFSFTYSTDEERAFVRELAALLASPL	120
QY	121	LIDAIQINPAY	132	
DB	121	LIDAIQINPAY	132	

RESULT 2
S01964
readthrough protein - phage SP
C:Species: phage SP
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

A/Title: Listeriolysin genes: complete sequence of ilo from *Listeria ivanovi* and of lsc
A/Reference number: S22340: MUID:92182018: PMID:1543752

A;Status: nucleic ac
A:Molecule type: DNA

A:Residues: 1-529 <RAS>
A:Cross-references: UNIPROT:P13128; EMBL:X60035; NID:g44110; PIDN:CAA42639.1; PID:g44112
A:Experimental source: strain 12067, serotype 4b
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C:Genetics:
A:Gene: 116A
C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-529/Product: listeriolysin #status predicted <MAT>
Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;
QY 13 RDGKQTLV-----NPRGVPTNGVASTLSOAG-----VPALEKRV 48
DB 93 KDGNEIIVVEKKKKSINQNNADIQVNNALISLTPGALVANSBELVENQPDVLPVKRDSL 152
QY 49 TVSVSOPSRNRKNKYQVQKIQNPACTANGSCDPSVTR-----QKYADYTFSTQYSTD 102
DB 153 TLSIDLPGMTNQNKILVVK--NATKSNVNNVAVTLVERNMEKXAQAQVNPVS---AKIDYD 207
QY 103 EERAFVPTIELAA 114
DB 208 DEMAYESBSQLIA 219
RESULT 7
A43505
Listeriolysin O precursor - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C:Accession: A43505; S05306; A47606; S12400; A61079
R:Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanzey
Intect. Immun. 56, 766-772, 1988
A:Title: Expression in *Escherichia coli* and sequence analysis of the listeriolysin O det
A:Reference number: A43505; PMID:88153053; PMID:3126142
A:Accession: A43505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <MEN>
A:Cross-references: UNIPROT:P13128; GB:M24199; NID:g149652; PIDN:AAA03018.1; PID:g149653
A:Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R:Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A:Title: Nucleotide sequence of the listeriolysin gene from a Listeria monocytogenes ser
A:Reference number: S05306; PMID:89366684; PMID:2505236
A:Accession: S05306
A:Molecule type: DNA
A:Residues: 1-529 <DOM>
A:Cross-references: EMBL:X15127; NID:g44106; PIDN:CAA3223.1; PID:g44107
A:Experimental source: strain EGD
A:Note: this sequence is derived from a weakly hemolytic strain, serotype 1/a
R:Mengaud, J.; Chenevert, J.; Geoffroy, C.; Gaillard, J.L.; Cossart, P.
Infect. Immun. 55, 3225-3237, 1987
A:Title: Identification of the structural gene encoding the SH-activated hemolysin of *L*
A:Reference number: A47606; PMID:88057627; PMID:2824384
A:Accession: A47606
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 413-480 <ME2>
A:Cross-references: GB:M29171
R:Michel, E.; Reisch, K.A.; Pavier, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A:Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtain
A:Reference number: S12400; PMID:91211627; PMID:1965218
A:Accession: S12400
A:Molecule type: DNA
A:Residues: 483-493 <MTC>
A:Experimental source: strain LO28, serotype 1/2c
C:Genetics:
A:Gene: hlyA; 116A

C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-529/Product: listeriolysin O #status predicted <MAT>
Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;
QY 13 RDGKQTLV-----NPRGVPTNGVASTLSOAG-----VPALEKRV 48
DB 93 KDGNEIIVVEKKKKSINQNNADIQVNNALISLTPGALVANSBELVENQPDVLPVKRDSL 152
QY 49 TVSVSOPSRNRKNKYQVQKIQNPACTANGSCDPSVTR-----QKYADYTFSTQYSTD 102
DB 153 TLSIDLPGMTNQNKILVVK--NATKSNVNNVAVTLVERNMEKXAQAQVNPVS---AKIDYD 207
QY 103 EERAFVPTIELAA 114
DB 208 DEMAYESBSQLIA 219
RESULT 8
AC1100
Listeriolysin O precursor (imported) - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1100
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fehl, H.,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maltournam, A.; Mat
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria* species
A:Reference number: AB1077; PMID:21537279; PMID:11679669
A:Accession: AC1100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <GIA>
A:Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:g16409567; GSPDB:C
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: hly
C:Superfamily: dipeptide transport protein
Query Match 12.3%; Score 81.5; DB 2; Length 529;
Best Local Similarity 22.0%; Pred. No. 4;
Matches 29; Conservative 24; Mismatches 44; Indels 35; Gaps 5;
QY 13 RDGKQTLV-----NPRGVPTNGVASTLSOAG-----VPALEKRV 48
DB 93 KDGNEIIVVEKKKKSINQNNADIQVNNALISLTPGALVANSBELVENQPDVLPVKRDSL 152
QY 49 TVSVSOPSRNRKNKYQVQKIQNPACTANGSCDPSVTR-----QKYADYTFSTQYSTD 102
DB 153 TLSIDLPGMTNQNKILVVK--NATKSNVNNVAVTLVERNMEKXAQAQVNPVS---AKIDYD 207
QY 103 EERAFVPTIELAA 114
DB 208 DEMAYESBSQLIA 219
RESULT 9
S57537
MKII protein - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein N2302; protein YNL085w
C:Species: *Saccharomyces cerevisiae*
C:Date: 10-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57537; S50279; S63024; S63017; S65096
R:Solier-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57533

A/Accession: S57537
 A/Molecule type: DNA
 A/Residues: 1-830 <SOL>
 A/Cross-references: UNIPROT:P40850; EMBL:X89016; NID:9887621; PID:9887626
 R/Vermut, M.; Widner, W.R.; Dismann, J.D.; Wickner, R.B.
 Yeast 10, 1477-1479, 1994
 A/Title: Sequence of MKT1, needed for propagation of M(2) satellite dsRNA of the L-A virus
 A/Reference number: S50279; MUID:95176705; PMID:7532890
 A/Accession: S50279
 A/Molecule type: DNA
 A/Residues: 1-29, 'G', 31-808, 'TWKTCIANYH' <VER>
 A/Cross-references: EMBL:U09129; NID:9520475; PIDN:AA049470.1; PID:9520476
 R/Soler-Mita, A.; Satz, J.E.; Ballesta, J.P.G.; Remacha, M.
 Submitted to the Protein Sequence Database, April 1996
 A/Reference number: S63018
 A/Accession: S63018
 A/Molecule type: DNA
 A/Residues: 1-830 <SOM>
 A/Cross-references: EMBL:Z71361; NID:91301982; PID:91301983; MIPS:YNL085W
 A/Experimental source: strain S288C
 R/Pohlmann, R.; Philippesen, P.
 Submitted to the Protein Sequence Database, April 1996
 A/Reference number: S62397
 A/Accession: S63017
 A/Molecule type: DNA
 A/Residues: 569-830 <POE>
 A/Cross-references: EMBL:Z71361; MIPS:YNL085W
 A/Experimental source: strain S288C
 R/Soler-Mita, A.; Satz, J.E.; Ballesta, J.P.G.; Remacha, M.
 Yeast 12, 485-491, 1996
 A/Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
 A/Reference number: S65092; MUID:96310628; PMID:8740422
 A/Accession: S65096
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-830 <SOF>
 A/Cross-references: EMBL:X89016; NID:9887621; PIDN:CAAC1425.1; PID:9887626
 C/Genetics:
 A/Gene: SGD:MKT1
 A/Cross-references: SGD:S0005029; MIPS:YNL085W
 A/Map position: 14L
 C/Superfamily: Saccharomyces cerevisiae MKT1 protein
 C/Keywords: transmembrane protein
 F:615-631/Domain: transmembrane #status predicted <TM>
 Query Match 12.2%; Score 81; DB 2; Length 830;
 Best Local Similarity 25.7%; Pred. No. 7.5;
 Matches 26; Conservative 20; Mismatches 49; Indels 6; Gaps 3;
 Oy 5 TTTTLCNCRDQKQTLVLPGRVNPPTNGVASSQAGVPALEKRVTVSVSOPSRRKRYKV 64
 Db 301 STTQNN--DSKENQNTQKISALRYPVLKDTGKVELFVQELVSEDESKNNKDK- 356
 Oy 65 QVKIQNPACTANGSCDPSVTRKQYADVTFSFTQYSTDEER 105
 Db 357 KSNLSSPS--SASSASAPATVTKASRKLTYEKSSTEVK 395
 RESULT 10
 RCBYH1
 C/CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
 N/Alternate names: protein L9672.1; protein YLR256W; regulatory protein CYP1; regulatory
 C/Species: Saccharomyces cerevisiae
 C/Date: 30-Sep-1991 #sequence_revision 23-Feb-1996 #text_change 12-Nov-1999
 C/Accession: S59400; A31312; S15447; S05804; S15446
 R/Johnson, D.
 submitted to the EMBL Data Library, February 1995
 A/Description: The sequence of S. cerevisiae cosmid 9672.
 A/Reference number: S59386
 A/Accession: S59400
 A/Molecule type: DNA
 A/Residues: 1-1502 <JOH>
 A/Cross-references: EMBL:U20865; NID:g662330; PIDN:AAB67387.1; PID:g662331; GSPDB:GN0001

A/Experimental source: strain S288C (AB972)
 R/Pfeifer, K.; Kim, K.S.; Kogan, S.; Guarente, L.
 Cell 56, 291-301, 1989
 A/Title: Functional dissection and sequence of yeast HAP1 activator.
 A/Reference number: A31312; MUID:89106221; PMID:2643482
 A/Accession: A31312
 A/Molecule type: DNA
 A/Residues: 1-144, 'T', 146-322, 'R', 324-454, 'N', 456-507, 'M', 509-586, 'K', 588-882, 'N', 884-951
 A/Cross-references: EMBL:U03152; NID:g171645; PIDN:AAA34662.1; PID:g171646
 R/Creusot, F.; Verdier, J.; Gaïgne, M.; Slonimski, P.P.
 J. Mol. Biol. 204, 263-276, 1988
 A/Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
 A/Reference number: S15447; MUID:89125585; PMID:2851658
 A/Accession: S15447
 A/Molecule type: DNA
 A/Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYRADPIME' <CRE1>
 A/Cross-references: EMBL:X13793
 A/Note: the sequence is from mutant CYP1-18
 C/Genetics:
 A/Gene: SGD:HAP1; CYP1; MIPS:YLR256W
 A/Cross-references: SGD:S0004246; MIPS:YLR256W
 A/Map position: 12R
 C/Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology
 C/Keywords: DNA binding; heme binding; transcription regulation; zinc finger
 F:1-148/Domain: DNA binding #status predicted <DNA>
 F:59-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F:64-84/Region: zinc finger CCCC motif
 F:177-189/Region: glutamine-rich
 F:245-445/Domain: heme binding #status predicted <HEM>
 F:299-304, 323-328, 347-352, 373-378, 389-394, 415-420/Region: 6-residue repeats
 F:1308-1481/Domain: activation element #status predicted <ACT>
 F:1388-1481/Region: acidic

Query Match 12.1%; Score 80.5; DB 1; Length 1502;
 Best Local Similarity 20.6%; Pred. No. 17;
 Matches 35; Conservative 30; Mismatches 42; Indels 63; Gaps 7;
 Oy 23 PRGVN--PTNGVAVSL-----SQAGVPALEKRVTVSVS 53
 Db 1278 PRGISPKSPKSGLSVQPLSSFSMNQNGSTIPVSLNTITSQMGALPSLDRTTNQIN 1337
 Oy 54 QPSRNR-KNYKVOVKIQNP-----TACTANGSCDP 82
 Db 1338 LPPPSRDEAFDNDISKQTPWTSAPMANNATTIPSTINGNNMAGTANTDTSANGSALS 1397
 Oy 83 SVTRKQKADY-TFSFTQYSTD-ERRAFVTRTELALASP-LTIDAIDQLN 129
 Db 1398 TLTPSQSDIANSATQYKPDLEDPLMOMNSFNGLMNPESLVEVVGYN 1447
 RESULT 11
 S22341
 I/vanolysin precursor - *Listeria ivanovii*
 C/Species: *Listeria ivanovii*
 C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
 C/Accession: S22341; S36683
 R/Haas, A.; Dumbeky, M.; Kreft, J.
 Biochim. Biophys. Acta 1130, 81-84, 1992
 A/Title: *Listeriolyisin* genes: complete sequence of *ilo* from *Listeria ivanovii* and of *leo*
 A/Reference number: S22340; MUID:92182018; PMID:11543752
 A/Accession: S22341
 A/Molecule type: DNA
 A/Residues: 1-528 <HNS>
 A/Cross-references: UNIPROT:P31831; EMBL:X60461
 A/Note: the authors translated the codon ACA for residue 331 as Val
 R/Kreft, J.
 submitted to the EMBL Data Library, July 1991
 A/Reference number: S36683
 A/Accession: S36683
 A/Molecule type: DNA
 A/Residues: 1-319, 'T', 321-528 <KRE>
 A/Cross-references: EMBL:X60461
 C/Genetics:

A:Gene: 110
C:Superfamily: dipeptide transport protein
F:1-24/Domains: signal sequence <Sig>
P:25-528/Product: Ivalnolysin #status predicted <Mtr>

Query Match 11.7%; Score 77.5; DB 2; Length 528;
Best Local Similarity 21.2%; Pred. No. 9.8;
Matches 28; Conservative 25; Mismatches 44; Indels 35; Gaps 5;
QY 13 RRGKQTLV-----NPRGVNPTNGVASLSQAGV-----VPALSKRY 48
DB 92 KEGNQITVEKKKKSINONNADIQVINSLSLTPGALVKANSELVENQPDVLPVKRDSY 151
QY 49 TVSVSQPSRRKRYKVQVXIONFTACTANGSCDPSVTR-----QKXADVTFSFTQSTD 102
DB 152 TISIDLP--GWNHDEIVQVNAKTSININDGVNLTLDNMNNKXSEYPNIS---AKIDVD 206
QY 103 EERAFVRETLAA 114
DB 207 QEWAYSESQLV 218

RESULT 12

131660
hypothetical protein COS41.6 - sea squirt (Cliona intestinalis)
C:Species: Clona intestinalis
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31660
R:Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Dobson, R.; Tweedie, S.
Submitted to the EMBL Data Library, December 1996
A:Reference number: Z21049
A:Accession: T31660
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-432 <RIR>
A:Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDN:CAB0605
C:Genetics:
A:introns: 180/2; 212/1; 229/3

Query Match 11.6%; Score 77; DB 2; Length 432;
Best Local Similarity 27.4%; Pred. No. 8.7;
Matches 31; Conservative 17; Mismatches 47; Indels 18; Gaps 6;
QY 4 ETVTLCNIGRDGKQTLVLPNGVNPNGVASLSQAGVPALEKRYTVSVSQPSRRKRYK 63
DB 242 DTSSEBEVTKDGGNLAENP---TPSNARELOESVASVLTETTVKSAIQ--EQDSAYR 257
QY 64 VQVKIQNPACTA--TANGSC-----DPSVTRQRYAD---VTFSTQYSTDE 103
DB 298 KE-NPQNAACPVRNNGNCVSTNSKTPNDISKIYVNSDDNTDDEDTQIDPTNE 349

RESULT 13

C98221
hypothetical protein AGR_1.1428 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: C98221
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2333-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; WUID:21608551; PMID:11743194
A:Accession: C98221
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <RUR>
A:Cross-references: UNIPROT:Q8UBF3; GB:AE007870; PIDN:AAK89293.1; PID:g15159127; GSPDB:G
C:Genetics:
A:Gene: AGR_1.1428
A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;

Best Local Similarity 24.6%; Pred. No. 2.5;
Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGRDGKQTLVLPNGVNPNGVASLSQAGV-----PALSKRYTVSVSQPSRRN 59
DB 3 ISKDGKQTSADPHWLEWVTGTISTLLVAMRWIYDIYRSPPEARFEIATVGEGQT 62
QY 60 KNYKVQVKIQNPACTA-----NGSCDPSVTRQRYADVTFSF--TOYSTDEERAFVTE 111
DB 63 GQYRVAFALHNSMTTAAQVNVVRGDLQNGASPEKNADVTFDYVASSKONGTLFFRSD 120

RESULT 14

AE3065
conserved hypothetical protein Atcu4139 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE3065
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavh, T.; Levy, R.; Li, M.; McCelliff
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, B.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; WUID:21608550; PMID:11743193
A:Accession: AE3065
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <RUR>
A:Cross-references: UNIPROT:Q8UBF3; GB:AE008689; PIDN:AAL44939.1; PID:g17742593; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atcu4139
A:Map position: linear chromosome

Query Match 11.5%; Score 76.5; DB 2; Length 136;
Best Local Similarity 24.6%; Pred. No. 2.5;
Matches 29; Conservative 16; Mismatches 56; Indels 17; Gaps 3;

QY 11 IGRDGKQTLVLPNGVNPNGVASLSQAGV-----PALSKRYTVSVSQPSRRN 59
DB 3 ISKDGKQTSADPHWLEWVTGTISTLLVAMRWIYDIYRSPPEARFEIATVGEGQT 62
QY 60 KNYKVQVKIQNPACTA-----NGSCDPSVTRQRYADVTFSF--TOYSTDEERAFVTE 111
DB 63 GQYRVAFALHNSMTTAAQVNVVRGDLQNGASPEKNADVTFDYVASSKONGTLFFRSD 120

RESULT 15

C64221
hypothetical 114K protein (Mgpa 3' region) - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: C64221; J00092; S18702; S18703
C:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.A.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; WUID:96026346; PMID:7569993
A:Accession: C64221
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1052 <TIGR>
A:Cross-references: UNIPROT:P22747; GB:U39696; GB:L43967; NID:g1045869; PID:g1045877; TIC
A:Experimental source: strain G-37
R:Ramaine, J.M.; Loechel, S.; Collier, A.M.; Barile, M.F.; Hu, P.C.
Gene 82, 259-267, 1989
A:Title: Nucleotide sequence of the Mgpa (mgp) operon of Mycoplasma genitalium and compa
A:Reference number: J00090; WUID:90060815; PMID:2583522
A:Accession: J00092
A:Molecule type: DNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-6
Perfect score: 664
Sequence: 1 AALEVTYTGANIGRDGKQTLV.....AALLASPLLDIAIDQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_spromt:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	98.6	132	1	COAT_BPOBE
2	655	98.6	133	1	AAM3126
3	655	98.6	329	2	Q8LTEL1
4	655	98.6	329	2	AAAI6663
5	564	84.9	133	2	Q9TOR9
6	564	84.9	133	2	Q64307
7	544	81.9	133	2	Q9TOS0
8	529.5	79.7	132	1	COAT_BPSP
9	529.5	79.7	132	1	COAT_BPSP
10	529.5	79.7	331	1	VAL_BPSP
11	496.5	74.8	132	2	Q9TOR8
12	496.5	74.8	330	2	Q64310
13	116	17.5	131	1	COAT_BPPRR
14	96.5	14.5	473	1	Q8VDC2
15	87.5	13.2	530	1	TACY_LISSB
16	87.5	13.2	530	2	AA897361
17	85.5	12.9	540	2	O48683
18	82.5	12.4	608	2	O84H79
19	82	12.3	325	2	Q73R79
20	82	12.3	325	2	AA810709
21	82	12.3	325	2	O6HGAT7
22	81.5	12.3	529	1	TACY_LISMF
23	81.5	12.3	529	1	TACY_LISMO
24	81.5	12.3	529	2	Q9L5B9
25	81.5	12.3	529	2	Q6E9A2
26	81.5	12.3	529	2	Q6E9A2
27	81.5	12.3	529	2	Q6E9G2
28	81.5	12.3	529	2	Q6E9G2
29	81.5	12.3	529	2	Q6E9T2
30	81.5	12.3	529	2	Q6E9A8
31	81.5	12.3	529	2	Q6E9A6

32	81.5	12.3	529	2	Q6E9A7	Q6e9a7 listeria mo
33	81.5	12.3	529	2	Q6E9A0	Q6e9a0 listeria mo
34	81.5	12.3	529	2	Q6E9A4	Q6e9a4 listeria mo
35	81.5	12.3	529	2	AAAT03000	AAAT03000 listeria
36	81	12.2	830	1	MKT1_YEAST	P40850 saccharomyc
37	81	12.2	830	2	O8TF87	O8tf87 saccharomyc
38	81	12.2	830	2	O8TF89	O8tf89 saccharomyc
39	81	12.2	830	2	O8TF45	O8tf45 saccharomyc
40	81	12.2	830	2	O8TF52	O8tf52 saccharomyc
41	81	12.2	830	2	O8TF55	O8tf55 saccharomyc
42	81	12.2	830	2	AAAO0519	AAAO0519 saccharom
43	81	12.2	1624	2	O9V3K8	O9v3k8 drosophila
44	81	12.2	1637	2	O9SRU8	O9srU8 drosophila
45	80.5	12.1	1502	1	CYPL_YEAST	P12351 saccharomyc

ALIGNMENTS

RESULT 1
ID COAT_BPOBE STANDARD; PRT; 132 AA.
AC P03615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievivirus.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clelens I., Drellina D., Dieler A., Baumann V.,
RA One V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
RL assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmis C., Sastre P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
RT bacteriophage Q-beta as an application of a mapping procedure for RNA
RL fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Stoll R., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
RT and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maiba T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundale M., Vallegard K., Lilljas L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
RN [6]
RP FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----

DR EMBL; M99039; AAA1662.1; -.

DR EMBL; V00643; CAA23992.1; -.

DR PIR; A92240; VCBPOB.

DR PDB; 1QBE; X-ray; A/B/C=1-132.

DR InterPro: IPR002703; Levi_coat.

DR Pfam; PF01819; Levi_coat; 1.

KW 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.

FT INIT MET 0 0

FT CONFLICT 22 22 N -> D (in Ref. 4).

FT CONFLICT 56 56 Missing (in Ref. 4).

FT STRAND 5 9

FT TURN 13 14

FT STRAND 18 27

FT TURN 28 31

FT STRAND 32 36

FT HELIX 42 44

FT STRAND 47 53

FT STRAND 56 58

FT TURN 57 58

FT STRAND 59 59

FT STRAND 62 74

FT STRAND 83 96

FT TURN 98 99

FT HELIX 102 117

FT HELIX 119 126

FT TURN 127 127

SEQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 98.6%; Score 655; DB 1; Length 132;

Best Local Similarity 98.5%; Pred. No. 8.6e-56;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKETVTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSNRK 60

DB 1 AKETVTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSNRK 60

QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVRLTAALLASPL 120

DB 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVRLTAALLASPL 120

QY 121 LIDAIDQLNPAV 132

DB 121 LIDAIDQLNPAV 132

RESULT 2

AAAM33126 PRELIMINARY; PRT; 133 AA.

ID AAAM33126

AC AAAM33126; (Tremblrel. 27, Created)

DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)

DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)

DE Coat protein.

OS Bacteriophage Q-beta.

CC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

CC Alilevivirus; Alilevivirus subgroup III.

OX NCBI_TaxID=12009;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=14667253;

RA Bacher J.M., Bull J.J., Ellington A.D.;

RT "Evolution of phage with chemically ambiguous proteomes.";

RL BMC Evol. Biol. 3:24-24(2003).

DR EMBL; AY099114; AAAM33126.1; -.

KW Coat protein.

SEQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.6%; Score 655; DB 2; Length 133;

Best Local Similarity 98.5%; Pred. No. 8.7e-56;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKETVTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSNRK 60

DB 2 AKETVTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSNRK 61

QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVRLTAALLASPL 120

DB 62 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVRLTAALLASPL 121

QY 121 LIDAIDQLNPAV 132

DB 122 LIDAIDQLNPAV 133

RESULT 3

Q8LTE1 PRELIMINARY; PRT; 329 AA.

ID Q8LTE1

AC Q8LTE1;

DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 05-JUN-2004 (Tremblrel. 27, Last annotation update)

DE A1 read-through protein (A1 protein).

OS Bacteriophage Q-beta.

CC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

CC Alilevivirus.

OX NCBI_TaxID=12009;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=14667253;

RA Bacher J.M., Bull J.J., Ellington A.D.;

RT "Evolution of phage with chemically ambiguous proteomes.";

RL BMC Evol. Biol. 3:24-24(2003).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=4109687; PubMed=7506687;

RA Kozlovskaya T.M., Clemons I., Drellima D., Dieters A., Baumanis V.,

RA Ose V., Pumpens P.;

RT "Recombinant RNA phage Q beta capsid particles synthesized and self-

RT assembled in Escherichia coli.";

RL Gene 137:133-137(1993).

DR EMBL; AY099114; AAAM33127.1; -.

DR EMBL; M99039; AAA1663.1; -.

DR HSP; P03615; IQBE.

DR GO; GO:0019028; C:Viral capsid; IEA.

DR GO; GO:0005198; F:Structural molecule activity; IEA.

DR InterPro: IPR002703; Levi_coat.

DR InterPro: IPR000504; RNA_Tec_mot.

DR Pfam; PF01819; Levi_coat; 1.

DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.

SEQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.6%; Score 655; DB 2; Length 329;

Best Local Similarity 98.5%; Pred. No. 2.5e-55;

Matches 130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKETVTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSNRK 60

DB 2 AKETVTLGNIGRDKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVQPSNRK 61

QY 61 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVRLTAALLASPL 120

DB 62 NYKVQVKIONPTACTANGSCDPSVTRQKADVTFSFTQYSTDBERAFVRLTAALLASPL 121

QY 121 LIDAIDQLNPAV 132

DB 122 LIDAIDQLNPAV 133

RESULT 4

AAAI6663 PRELIMINARY; PRT; 329 AA.

ID AAI6663

AC AAI6663;

DT 02-MAR-2004 (Tremblrel. 27, Created)


```
DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirinae.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielens I., Dreilima D., Dislers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; M99039; AAA1663.1; -;
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.6%; Score 655; DB 2; Length 329;
Best Local Similarity 98.5%; Pred. No. 2.5e-55;
Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVQPSRNRK 60
DB 2 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVQPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAAALASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAAALASPL 121
QY 121 LIDAIQDNLNPAY 132
DB 122 LIDAIQDNLNPAY 133

RESULT 5
QYTOR9 PRELIMINARY; PRT; 133 AA.
AC QYTOR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirinae.
OX NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14699.1; -.
DR HSP; P03615; IQBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 2559593DA6F6474 CRC64;
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Query Match 84.9%; Score 564; DB 2; Length 133;
Best Local Similarity 82.6%; Pred. No. 6.3e-47;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVQPSRNRK 60
DB 2 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVQPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAAALASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAAALASPL 121
QY 121 LIDAIQDNLNPAY 132
DB 122 LIDAIQDNLNPAY 133

RESULT 6
QYTOR9 PRELIMINARY; PRT; 329 AA.
AC QYTOR9;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirinae.
OX NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder M.J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14700.1; -.
DR HSP; P03615; IQBE.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 84.9%; Score 564; DB 2; Length 329;
Best Local Similarity 82.6%; Pred. No. 1.8e-46;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVQPSRNRK 60
DB 2 AKLETVTLGNIGDGGKQTLVLRGNVPTNGVSLSGAGVPALEKRVTVSVQPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAAALASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDERAFVRLTAAALASPL 121
QY 121 LIDAIQDNLNPAY 132
DB 122 LIDAIQDNLNPAY 133
```

```

RESULT 7
Q9T0S0 PRELIMINARY; PRT; 133 AA.
AC Q9T0S0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Coat protein.
OS Bacteriophage M1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
NCBI_TaxID=74336;
OX NCBI_TaxID=74336;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
[3]
RN
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 098722E3C6C3A255 CRC64;

Query Match 81.9%; Score 544; DB 2; Length 133;
Best Local Similarity 79.5%; Pred. No. 5.6e-45;
Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRYTVSVSOPSRRNK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 AKLQAITLSGIGKGGVTLIDLPNGVNPPTNGVAAISEAGVPALEKRYTVISVOPSRRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRKYADVTFSTQYSTDEERAFVTELAALASPL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 NYKVQVKIQNPACTANGSCDPSVTRKYADVTFSTQYSTDEERAFVTELAALADPM 121
QY 121 LIDALDQNPAY 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 LVNALDNLNPAY 133

RESULT 8
Q64303 PRELIMINARY; PRT; 329 AA.
AC Q64303;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
NCBI_TaxID=74336;
OX NCBI_TaxID=74336;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
[3]
RN
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06251.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RNP_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35893 MW; 3E33CD821E8625F4 CRC64;

Query Match 81.9%; Score 544; DB 2; Length 329;
Best Local Similarity 79.5%; Pred. No. 1.6e-44;
Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRYTVSVSOPSRRNK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 AKLQAITLSGIGKGGVTLIDLPNGVNPPTNGVAAISEAGVPALEKRYTVISVOPSRRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRKYADVTFSTQYSTDEERAFVTELAALASPL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 NYKVQVKIQNPACTANGSCDPSVTRKYADVTFSTQYSTDEERAFVTELAALADPM 121
QY 121 LIDALDQNPAY 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 LVNALDNLNPAY 133

RESULT 9
COAT BPSP STANDARD; PRT; 132 AA.
ID COAT BPSP
AC P06673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
NCBI_TaxID=12027;
OX NCBI_TaxID=12027;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirasima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC 1-1 FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
CC DR EMBL; X07489; CA30374.1; -.
CC HSSP; P03615; IOBE.

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DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
KW Coat protein; RNA-binding.
SQ SEQUENCE 132 AA; 14129 MW; 50B1E6CC6AF0A254 CRC64;

Query Match 79.7%; Score 529.5; DB 1; Length 132;
Best Local Similarity 78.0%; Pred. No. 1.4e-43;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 AKLETVTLGNGIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVQPSNRK 60
DB 2 AKLNQVTLSTIGKNGKGDQTLITPRGVNPTNGVASLSRAGVPALEKRVTVSVQPSNRK 61
QY 61 NYKVQVQIQLQNPACTANGSCDPSVTRKQYADVTFSTQYSTDEERARVTELAAALASPL 120
DB 62 NFKVQIQLQNPACTRQD-ACDPSVTRSAFADVTLSTFTSYSTDEERALLRTELAAALADPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 IVDADIDNLNPAY 132

RESULT 10
VAL_BPSP STANDARD; PRT; 331 AA.
ID VAL_BPSP
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Readthrough protein A1 [Contains: Coat protein].
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC NCBI_TaxID=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hiraehima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
CC protein sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: X07489; CAB37299.1; -.
DR PIR: S01964; S01964.
DR HSSP: P03615; IOBE.
DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
KW Coat protein.
FT CHAIN 1 132 Coat protein.
FT CHAIN 1 331 Readthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A642E34B52C6582 CRC64;

Query Match 79.7%; Score 529.5; DB 1; Length 331;
Best Local Similarity 78.0%; Pred. No. 4.2e-43;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 AKLETVTLGNGIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVQPSNRK 60
DB 2 AKLNQVTLSTIGKNGKGDQTLITPRGVNPTNGVASLSRAGVPALEKRVTVSVQPSNRK 61
QY 61 NYKVQVQIQLQNPACTANGSCDPSVTRKQYADVTFSTQYSTDEERARVTELAAALASPL 120
DB 62 NFKVQIQLQNPACTRQD-ACDPSVTRSAFADVTLSTFTSYSTDEERALLRTELAAALADPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 IVDADIDNLNPAY 132
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DB 62 NFKVQIQLQNPACTRQD-ACDPSVTRSAFADVTLSTFTSYSTDEERALLRTELAAALADPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 IVDADIDNLNPAY 132

RESULT 11
Q9TOR8 PRELIMINARY; PRT; 132 AA.
ID Q9TOR8
AC Q9TOR8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC NCBI_TaxID=75725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF059243; AAC14703.1; -.
DR HSSP: P03615; IOBE.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR002703; Lev1_coat.
DR Pfam: PF01819; Lev1_coat; 1.
KW Coat protein.
SQ SEQUENCE 132 AA; 14143 MW; 672709375F5F22EA CRC64;

Query Match 74.8%; Score 496.5; DB 2; Length 132;
Best Local Similarity 75.0%; Pred. No. 2.3e-40;
Matches 99; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 1 AKLETVTLGNGIGRDGKQTLVLPNGVNPPTNGVASLSQAGVPALEKRVTVSVQPSNRK 60
DB 2 AKLNQVTLSTIGKNGKGDQTLITPRGVNPTNGVASLSRAGVPALEKRVTVSVQPSNRK 61
QY 61 NYKVQVQIQLQNPACTANGSCDPSVTRKQYADVTFSTQYSTDEERARVTELAAALASPL 120
DB 62 NFKVQIQLQNPACTRQD-ACDPSVTRSGSRDVTLSFTSYSTDEERALLRTELAAALADPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 IVDADIDNLNPAY 132

RESULT 12
O64310 PRELIMINARY; PRT; 330 AA.
ID O64310
AC O64310;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
```

OC Allollevivirus.
 OX NCBI_TaxID=75725;
 RN
 SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta."
 RL J. Mol. Biol. 247:903-917(1995).
 RN
 SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RL J. Mol. Biol. 256:8-19(1996).
 RN
 SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -
 DR HSSP; P03615; 10BE.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1 coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Lev1_coat_1; UNKNOWN.1.
 DR PROSITE; PS00030; RRM_RNP_1; 961E55F40834410 CRC64;
 SQ SEQUENCE 330 AA; 36175 MW; 961E55F40834410 CRC64;
 Query Match 74.8%; Score 496.5; DB 2; Length 330;
 Best Local Similarity 75.0%; Pred. No. 6.8e-40;
 Matches 99; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKLETVTGNIGRDGKQTLV--LNPRGVNPTNGV--VASISQAGVPALEKRYTVSVSQPSNRK 60
 DB 2 AKLNKVTLTGIGKAGNQTLTLTPRGVNPENGVASISEAGVPALEKRYTVSVSQPSNRK 61
 QY 61 NYKQVQKQNPCTANGSCDPSVTRKXAVTVTSFTQYSDERAFVTELAALASPLI 120
 DB 62 NYKQVQKQNPCTANGSCDPSVTRKXAVTVTSFTQYSDERAFVTELAALASPLI 120
 QY 121 LIDAIQDLPAY 132
 DB 121 IVDALDINLPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR STANDARD; PRT; 131 AA.
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OX NCBI_TaxID=12024;
 RN
 SEQUENCE.
 RP MEDLINE=79148387; PubMed=107028;
 RA Dhasee P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PR1."
 RL Eur. J. Biochem. 94:375-386(1979).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR PIR; A04225; VCBP1.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat_1.
 KW Coat protein; Direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7B639E1E50FC612 CRC64;
 OC

Query Match 17.5%; Score 116; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0025;
 Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;
 QY 17 QTLVLPNGVNP-----NGVASISQAGVPALEKRYTVSVSQPSNRKRYVQV 66
 DB 4 QNLVLDKRETPDHPDFPRDIDNNGEVESGVPGESRFTSLKTSNGR--YKSTL 61
 QY 67 KIQNPT--ACTANGSCDPSVTRKXAVTVTSFTQYSDERAFVTELAALASPLI 122
 DB 62 KLVVPVQSQTVNGIYVTPVVRISYTVDPDYDARSTTKERNPFGVGIADALADLVLV 121
 QY 123 DAIDQDLPAY 132
 DB 122 DTIVNLQGVY 131
 RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2 PRELIMINARY; PRT; 473 AA.
 AC Q8VDC2;
 DT 01-MAR-2002 (TRENBERE1, 20, Created)
 DT 01-MAR-2002 (TRENBERE1, 20, Last sequence update)
 DT 01-OCT-2003 (TRENBERE1, 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Tmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN
 SEQUENCE FROM N.A.
 RP STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kiss H., Darai E., Kiss C., Kost-Alimova M., Klein G., Dumanski J.P.,
 RA Imreh S.;
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3."
 RL Mamm. Genome 13:646-655 (2002).
 DR EMBL; AJ428064; CAD20986.1; -
 DR MGD; MGI:2446841; Tmem7.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0E69F2A4D CRC64;
 Query Match 14.5%; Score 96.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 0.9; Indels 69; Gaps 7;
 Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;
 QY 5 TTTTGNIGRDGKQTLV-----LNPRGVNPTNG--VASISQAGVPALEKRYTVSVSQPSNRKRYVQV 46
 DB 195 TATCSNLSISSQSPSSKQVQPKASKANPQASNTKNDPVKSCSKPAPPLSPSLKSAREP 254
 QY 47 RYTVSVSQPSNRKRYVQV-----KIQNPT--ACTANGSCDPSVTRQ----- 87
 DB 255 KYTVTCNLSISSSSSSSKQVQPKASKANPQASNTKNDPVKSCSKPAPPLSPSLKSAREP 314
 QY 88 -----KYADVTFTQYSDERAFVTELAALASPLI 122
 DB 315 SPAPAPCTVQMPSPPTIDSGRADVAKENTRSKTRK-----ALLSSPLYV 361
 RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE STANDARD; PRT; 530 AA.
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligeriolysin precursor (Thiol-activated cytolysin).
 GN Name=Isol;
 OS Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

[illegible]

Search completed: January 4, 2005, 09:16:15
Job time : 37.2676 secs

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OM protein - protein search, using SW model

Run on: January 4, 2005, 08:56:31 ; Search time 98.9054 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-4

Perfect score: 1749
Sequence: 1 MAKLETVLGNIGKDGKQTL.....FTKPKTKCP1QAVIVPRA 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*\n2: Geneseqp1980s:*\n3: Geneseqp2000s:*\n4: Geneseqp2001s:*\n5: Geneseqp2002s:*\n6: Geneseqp2003as:*\n7: Geneseqp2003bs:*\n8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1749	100.0	329	5	ABG94278 Bacterioph
2	1749	100.0	329	5	ABG80590 Bacterioph
3	1749	100.0	329	6	ABU09687 Bacterioph
4	1749	100.0	329	7	ADD24118 Bacterioph
5	1749	100.0	329	7	ADJ82044 Protein f
6	1749	100.0	329	7	ADK17132 Virus-11k
7	1749	100.0	329	8	ADJ36301 Bacterioph
8	1749	100.0	329	8	ADJ67147 Bacterioph
9	1749	100.0	329	8	ADK52181 Bacterioph
10	1733.5	99.1	328	6	ABR56440 Bacterioph
11	1733.5	99.1	328	6	ABR44543 Bacterioph
12	978	55.9	329	6	ABR56445 Bacterioph
13	978	55.9	329	6	ABR44548 Bacterioph
14	978	55.9	329	7	ADD24123 Bacterioph
15	978	55.9	329	7	ADJ82049 Protein f
16	978	55.9	329	7	ADK17137 Virus-11k
17	978	55.9	329	8	ADJ36306 Bacterioph
18	978	55.9	329	8	ADJ67152 Bacterioph
19	978	55.9	329	8	ADK52186 Bacterioph
20	978	55.9	330	5	ABG94315 RNA phage
21	976.5	51.3	331	5	ABG80627 Bacterioph
22	897.5	51.3	330	5	ABG94241 Bacterioph
23	897.5	51.3	330	5	ABG80553 Bacterioph
24	897.5	51.3	330	6	ABR56449 Bacterioph
25	897.5	51.3	330	6	ABR44552 Bacterioph

26	897.5	51.3	330	7	ADD24127 Bacterioph
27	897.5	51.3	330	7	ADJ82053 Protein f
28	897.5	51.3	330	7	ADK17141 Virus-11k
29	897.5	51.3	330	8	ADJ36310 Enterobac
30	897.5	51.3	330	8	ADJ67156 Bacterioph
31	897.5	51.3	330	8	ADK52190 Enterobac
32	663	37.9	132	5	ABG94233 Bacterioph
33	663	37.9	132	5	ABG80545 Bacterioph
34	663	37.9	132	6	ABR56439 Bacterioph
35	663	37.9	132	6	ABU09686 Bacterioph
36	663	37.9	132	6	ABR44542 Bacterioph
37	663	37.9	132	7	ADD24117 Bacterioph
38	663	37.9	132	7	ADJ82043 Protein f
39	663	37.9	132	7	ADK17131 Virus-11k
40	663	37.9	132	8	ADJ36300 Bacterioph
41	663	37.9	132	8	ADJ67146 Bacterioph
42	663	37.9	132	8	ADK52180 Bacterioph
43	655	37.4	132	5	ABG94316 POB240 pr
44	655	37.4	132	5	ABG94320 POB251 pr
45	655	37.4	132	5	ABG80632 Bacterioph

ALIGNMENTS

RESULT 1	ABG94278	standard, protein, 329 AA.
ID	ABG94278	
XX	ABG94278;	
AC	06-AUG-2003 (revised)	
DT	10-DEC-2002 (first entry)	
DT	10-DEC-2002	
XX		
DE	Bacteriophage Q beta coat protein Al.	
XX		
KW	Human; mouse; rat; antitubercular; antiallergic; immunomodulatory;	
KW	cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;	
KW	vaccine; infectious disease.	
XX		
OS	Bacteriophage.	
XX		
PN	WO200256905-A2.	
XX		
PD	25-JUL-2002.	
XX		
PF	21-JAN-2002; 2002MO-IB000166.	
XX		
PR	19-JAN-2001; 2001US-0262379P.	
PR	04-MAY-2001; 2001US-0286549P.	
PR	05-OCT-2001; 2001US-0326998P.	
PR	07-NOV-2001; 2001US-0331045P.	
XX		
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
XX		
PI	Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;	
PI	Ploesek C;	
XX		
DR	WPI; 2002-627351/67.	
XX		
PT	Molecular antigen array used in the production of vaccines for infectious	
PT	diseases.	
XX		
PS	Claim 7; Page 416-417; 44pp; English.	
XX		
CC	This invention relates to a novel ordered and repetitive antigen array	
CC	used in the production of vaccines for infectious diseases. The invention	
CC	also discloses a composition comprising a non-natural molecular scaffold	
CC	comprising a core particle selected from a core particle of a non-natural	
CC	origin and a core particle of natural origin and an organism comprising	
CC	at least one first attachment site, where the organism is connected to	
CC	the core particle by at least one covalent bond. Also disclosed is an	
CC	antigen or antigenic determinant with at least one second attachment	

site, where the antigen or antigenic determinant is any/old beta peptide (Abeta1-42) or its fragment and where the second attachment site is selected from an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Qbeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention. (Updated on 06-AUG-2003 to correct OS field.)

Sequence 329 AA;

Query Match	100.0%	Score 1749;	DB 5,	Length 329;
Best Local Similarity	100.0%;	Pred. No. 3e-171;		
Matches 329; Conservative	0;	Mismatches	0;	Gaps 0;

Qy	1	MAKLETVTLGNIGKQKQKQTLVNPBRVNPVTNGVASLSQAGAVALEKRYTVSVSQSRNR	60
Db	1	MAKLETVTLGNIGKQKQKQTLVNPBRVNPVTNGVASLSQAGAVALEKRYTVSVSQSRNR	60
Qy	61	KNYKQVQKQNPFPACTANGSCDPSVTRQAYADVTBFTQYSNDBEERAFRTETLAAALASP	120
Db	61	KNYKQVQKQNPFPACTANGSCDPSVTRQAYADVTBFTQYSNDBEERAFRTETLAAALASP	120
Qy	121	LIIIDAIDQNPWYWTLLIAGGSGSGSRPDPVIPPDPIDPPRGTKYKCPFAIWSLEEVYEB	180
Db	121	LIIIDAIDQNPWYWTLLIAGGSGSGSRPDPVIPPDPIDPPRGTKYKCPFAIWSLEEVYEB	180
Qy	181	PKNRNRPPIYNAVELOPREFDVALKOLLGNTKTRKMDSRSLSTYTFPGRCRNGYIIDIDATY	240
Db	181	PKNRNRPPIYNAVELOPREFDVALKOLLGNTKTRKMDSRSLSTYTFPGRCRNGYIIDIDATY	240
Qy	241	IATDQMRQOKDIREGKKPFAFGNIERTFYILKSINAYCSLSDIAVHADGVIVGEWRDP	300
Db	241	IATDQMRQOKDIREGKKPFAFGNIERTFYILKSINAYCSLSDIAVHADGVIVGEWRDP	300
Qy	301	SSGGAIPEPDTFKDKTKCPIQAVIVVPRRA	329
Db	301	SSGGAIPEPDTFKDKTKCPIQAVIVVPRRA	329

RESULT 2

ID ABG80590 standard; protein; 329 AA.

AC ABG80590;

AA	29-AUG-2003	(revised)
DT	29-NOV-2002	(first entry)
DT	29-NOV-2002	(first entry)

Bacteriophage Q-beta A1 protein.

XX Molecular antigen array; vaccine; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; AIDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myaesthesia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.

XX
PN W0200256907-A2.

PD 25-JUL-2002

PF 21-JAN-2002; 2002WO-IB000168.

PR 19-JAN-2001; 2001US-0262379P.

PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.

XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG

PA (MAUR/) MAURER P.

PA (ORTM/) ORTMANN R.

PA (STAU/) STAUFENBIEL M.

XX	Lechner F	Ortmann
RT	Mauver B	

Pl Renner WA, Bacchmann M, 11550
XX

NET, 2002-00001/00,
DN
XX

PT diseases.

PS Disclosure; Page 393-394; 418p.

CC The invention relates to a com
CC molecular scaffold comprising:

origin: and (ii) an organism comprising at least one first attachment

Molecular antigen array used in the production of vaccines for infectious diseases.

Disclosure; Page 393-394; 418pp; English.

The invention relates to a composition comprising: (a) a non-natural molecular scaffold comprising: (1) a core particle selected from: (1) a core particle of a non-natural origin; and (2) a core particle of natural origin; and (1) an organiser connected to the core particle by at least one covalent bond; (b) an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (A β eta 1-42) or its fragment, and where the second attachment site is selected from: (1) an attachment site not naturally occurring with the antigen or antigenic determinant; and (11) an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site; and where the antigen or antigenic determinant and the scaffold interact. Also included is a process for producing a non-naturally occurring ordered and repetitive antigen array. The composition is used in immunisation and as a vaccine for diseases such as influenza, gripp versus host disease, Igr-mediated allergic reactions, anaphylaxis, adult respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease, systemic lupus erythematosus, inflammatory immune disease, myasthenia gravis, immunoproliferative disease lymphadenopathy, rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease, angiodysplasia, infectious diseases. The antigens are modified to possess osteoporosis and infectious diseases. The antigens are modified to possess a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N- or C-terminal linker peptide which serves as the attachment point to a virus like particle or bacterial protein (the scaffold protein). The present sequence is bacterial protein or peptide which is coupled to the modified antigen to form the molecular antigen array. (Updated on 29-Aug-2003 to standardise OS field)

SQ Sequence 329 AA

Query Match	100.0%;	Score 1749;	DB 5;	Length 329;
Best Local Similarity	100.0%;	Pred. No. 3e-171;		
Matches 329; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

[illegible]


```

QY 61 KNYKVQVQKIQNTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRELAALLASP 120
DB 61 KNYKVQVQKIQNTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRELAALLASP 120
QY 121 LIIDAIDQINPQVWTLTLAGGSGSKPDVPIPDPIPPGKGKTCPPAIVSLSEVEVP 180
DB 121 LIIDAIDQINPQVWTLTLAGGSGSKPDVPIPDPIPPGKGKTCPPAIVSLSEVEVP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLATY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLATY 240
QY 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
DB 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329

RESULT 3
ABU09687 standard; protein; 329 AA.
ID ABU09687
AC ABU09687;
DT 03-JUL-2003 (first entry)
XX
DE Bacteriophage Qbeta coat protein A1.
XX
KM Bacteriophage Qbeta; coat protein; A1; hypotensive; cerebroprotective;
KM cardiant; nephroretroic; ophthalmological; immunostimulant; vaccine;
KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KM renin-activated angiotensin system; hypertension; stroke; infarction;
KM congestive heart failure; kidney failure; retinal haemorrhage.
XX
OS Bacteriophage Qbeta.
XX
PN WO2003031466-A2.
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-EP011219.
XX
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 19-JUL-2002; 2002US-0396637P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
P1 Bachmann M;
XX
DR WPI; 2003-430264/40.
XX
PT New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety, useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
XX
PS Claim 16; Page 92-93; 97pp; English.
XX
CC The invention describes an angiotensin peptide moiety carrier conjugate
CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal

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CC haemorrhage. The conjugate is also useful for inducing immune response,
CC including producing antibodies. This is the amino acid sequence of
CC bacteriophage Qbeta coat protein A1 used in the preparation of the
CC vaccine conjugates of the invention
XX
SQ Sequence 329 AA;
Query Match 100.0%; Score 1749; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MAKETVTLGNIGKQKOTIVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSNR 60
1 KAKETVTLGNIGKQKOTIVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSNR 60
61 KNYKVQVQKIQNTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRELAALLASP 120
61 KNYKVQVQKIQNTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRELAALLASP 120
DB 61 KNYKVQVQKIQNTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRELAALLASP 120
QY 121 LIIDAIDQINPQVWTLTLAGGSGSKPDVPIPDPIPPGKGKTCPPAIVSLSEVEVP 180
DB 121 LIIDAIDQINPQVWTLTLAGGSGSKPDVPIPDPIPPGKGKTCPPAIVSLSEVEVP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLATY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLATY 240
QY 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
DB 241 LATDQAMRDQKDIIEGKKPGAFGNIERFIYKLSINAYCSLSIDIAVHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329

RESULT 4
ADD24118
ID ADD24118 standard; protein; 329 AA.
XX
AC ADD24118;
XX
DT 15-JAN-2004 (first entry)
XX
DE Bacteriophage Qbeta coat protein A2.
XX
KM vaccine composition; virus-like particle; core particle;
KM first attachment site; antigen; antigenic determinant; prion protein;
KM PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
KM prion disease; Bovine Spongiform Encephalopathy; BSE;
KM Creutzfeldt-Jakob Disease; coat protein.
XX
OS Bacteriophage Qbeta.
XX
PN WO2003059386-A2.
PD 24-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-EP000460.
XX
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 08-JUL-2002; 2002US-0393725P.
PR 18-JUL-2002; 2002US-0396590P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
P1 Bachmann M, Maurer P, Pelliccioli E, Renner WA;
XX
DR WPI; 2003-598483/56.
XX
PT A vaccine composition for preventing or treating prion diseases (e.g.
PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-

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PT phage) and at least one prion protein or peptide bound to the virus-like
PT particle.
PS Disclosure; SEQ ID NO 11; 246pp; English.
XX
XX
XX This invention relates to a novel vaccine composition comprising a virus-
CC like or a core particle with at least one first attachment site and at
CC least one antigen or antigenic determinant that is a prion protein (Prp)
CC or its dimer, or a Prp peptide, the antigen or antigenic determinant
CC being bound to the virus-like or core particle. The vaccine of the
CC invention may have neuroprotective or antiinflammatory activity. The
CC composition is useful as a medicament or in manufacturing a medicament
CC for the treatment or prevention of prion diseases. The prion diseases may
CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
CC disease. The present sequence is the amino acid sequence of a coat
CC protein from a bacteriophage which may be used during the creation of the
CC vaccine composition of the invention.
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1749; DB 7; Length 329;
Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKLETVTLGNIGKQKQTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRRR 60
DB 1 MAKLETVTLGNIGKQKQTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRRR 60
QY 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTESFTQYSTDEBERAFVTEIAALLASP 120
DB 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTESFTQYSTDEBERAFVTEIAALLASP 120
QY 121 LIIDAIDQINPAWTLIIAGGSGSKPDPIPPDPPTGGTKYCPFAIMSLSEVYEP 180
DB 121 LIIDAIDQINPAWTLIIAGGSGSKPDPIPPDPPTGGTKYCPFAIMSLSEVYEP 180
QY 181 PTKNRPPPIYNAVEIQPREFDVALKDLGNTKWRDWSRLSYTTFRCGNGYIDLDATY 240
DB 181 PTKNRPPPIYNAVEIQPREFDVALKDLGNTKWRDWSRLSYTTFRCGNGYIDLDATY 240
QY 241 LATDQAMROKQDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRDP 300
DB 241 LATDQAMROKQDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRDP 300
QY 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329

RESULT 5
ADJ82044
ID ADJ82044 standard; protein; 329 AA.
AC ADJ82044;
XX
XX 06-MAY-2004 (first entry)
DE Protein for RANKL antigen array to treat bone disease.
XX
XX osteopathic; vaccine; core particle; antigenic determinant; RANKL;
KW bone disease; encephalopathy; immune system stimulation.
XX
XX Unidentified.
XX
XX MO2003039225-A2.
XX
XX 15-MAY-2003.
XX
XX 07-NOV-2002; 2002MO-EP012449.
XX
XX 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-IB000166.

PR 19-JUL-2002; 2002US-0396635P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M, Maurer P, Spohn G;
PI WPI; 2003-441430/41.
XX
XX
XX New compositions comprising a core particle and at least one antigen or
PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
PT of bone diseases, particularly mammalian encephalopathies.
XX
XX Disclosure; SEQ ID NO 11; 222pp; English.
XX
XX
XX The invention relates to a composition comprising a core particle having
CC at least one first attachment site, and at least one antigen or antigenic
CC determinant having at least one second attachment site. The antigen or
CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
CC peptide. The second attachment site is (non-) naturally occurring with
CC the antigen or antigenic determinant, and is capable of association to
CC the first attachment site. The antigen or antigenic determinant and the
CC core particle interact through the association to form an ordered and
CC repetitive antigen array. The composition is useful as a medicament, or
CC for the manufacture of a medicament for treating bone diseases. The
CC composition is especially useful for as a vaccine for therapy or
CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
CC and for stimulating mammalian immune system. This sequence represents a
CC protein of the invention.
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1749; DB 7; Length 329;
Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKLETVTLGNIGKQKQTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRRR 60
DB 1 MAKLETVTLGNIGKQKQTLVINPRGVNPTNGVASLSQAGAVPALEKRVTVSVQPSRRR 60
QY 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTESFTQYSTDEBERAFVTEIAALLASP 120
DB 61 KNYKQVQKIQNPACTANGSCDPSVTRQAYADVTESFTQYSTDEBERAFVTEIAALLASP 120
QY 121 LIIDAIDQINPAWTLIIAGGSGSKPDPIPPDPPTGGTKYCPFAIMSLSEVYEP 180
DB 121 LIIDAIDQINPAWTLIIAGGSGSKPDPIPPDPPTGGTKYCPFAIMSLSEVYEP 180
QY 181 PTKNRPPPIYNAVEIQPREFDVALKDLGNTKWRDWSRLSYTTFRCGNGYIDLDATY 240
DB 181 PTKNRPPPIYNAVEIQPREFDVALKDLGNTKWRDWSRLSYTTFRCGNGYIDLDATY 240
QY 241 LATDQAMROKQDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRDP 300
DB 241 LATDQAMROKQDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAVHADGVIYGVWRDP 300
QY 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329

RESULT 6
ADK17132
ID ADK17132 standard; peptide; 329 AA.
AC ADK17132;
XX
XX 06-MAY-2004 (first entry)
DE Virus-like particle repetitive antigen array peptide #11.
XX
XX antiallergic; antiaschemic; cytostatic; vaccine; virus-like particle;
KW interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX OS unidentified.
XX PN WO2003040164-A2.
XX 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-EP012455.
XX PR 07-NOV-2001; 2001US-0331045P.
XX PR 18-JAN-2002; 2002US-00050902.
XX PR 21-JAN-2002; 2002WO-1B000166.
XX PR 19-JUL-2002; 2002US-0396636P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PI Bachmann M, Jennings G, Sonderegger I;
XX DR WPI; 2003-441518/41.
XX PT Composition comprising an ordered and repetitive antigen or antigenic
XX PT determinant array, useful as a medicament, or for manufacturing a
XX PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
XX PT Hodgkin's lymphoma.
XX PS Disclosure; SEQ ID NO 11; 245bp; English.
XX CC The invention relates to a composition comprising a virus-like particle
XX CC and at least one antigen, which is a protein or peptide of interleukin
XX CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
XX CC core particle with at least one first attachment site and at least one
XX CC antigen with at least one second attachment site, where the antigen is a
XX CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
XX CC is an attachment site naturally occurring with the
XX CC antigen or antigenic determinant. The second attachment site is capable
XX CC of association to the first attachment site, and where the antigen or
XX CC antigenic determinant and the core particle interact through the
XX CC association to form an ordered and repetitive antigen array. The
XX CC compositions are useful as medicaments, or for manufacturing a medicament
XX CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
XX CC Hodgkin's lymphoma and related diseases. This sequence is used to
XX CC generate the compound of the invention.
XX SQ Sequence 329 AA;
Query Match 100.0%; Score 1749; DB 7; Length 329;
Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRTLAALLASP 120
61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRTLAALLASP 120
121 LIIDAIDQINPQYWTLLIAGGSGSKPDVIPPDPIDPPGKGKTCFPAIWSLEEVYEP 180
121 LIIDAIDQINPQYWTLLIAGGSGSKPDVIPPDPIDPPGKGKTCFPAIWSLEEVYEP 180
181 PTKNRPWPIYNAVELOPREFDVALKDLGNTKMRWDSRLSTTTRGCGNGYIDLDAFY 240
181 PTKNRPWPIYNAVELOPREFDVALKDLGNTKMRWDSRLSTTTRGCGNGYIDLDAFY 240
241 LATDQAMBDQKYDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
241 LATDQAMBDQKYDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
301 SSGGAIIPDFTKDKCPICQAVIVPRA 329
301 SSGGAIIPDFTKDKCPICQAVIVPRA 329

RESULT 7
ADJ36301
ID ADJ36301 strandad, protein; 329 AA.
XX AC ADJ36301;
XX DT 22-APR-2004 (first entry)
XX DE Bacteriophage Qbeta coat protein API protein subunit.
XX KW antiallergic; cytosatic; virucide; immunostimulant; vaccine;
XX KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
XX KW chronic disease; chronic viral disease; bacteriophage Qbeta;
XX KW coat protein; VLP; adjuvant; API coat protein.
XX OS Bacteriophage Qbeta.
XX PN WO2004000351-A1.
XX PD 31-DEC-2003.
XX PF 20-JUN-2003; 2003WO-EP006541.
XX PR 20-JUN-2002; 2002US-0389898P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PI Bachman MF, Renner WA;
XX DR WPI; 2004-108361/11.
XX PT New compositions comprising a virus-like particle (VLP), an
XX PT immunostimulatory substance bound to the VLP, and an antigen mixed with
XX PT the VLP, useful for enhancing immune response or for treating e.g. tumors
XX PT or chronic viral diseases.
XX PS Disclosure; SEQ ID NO 2; 252bp; English.
XX CC The invention describes a composition for enhancing an immune response in
XX CC an animal comprising a virus-like particle, an immunostimulatory
XX CC substance bound to the virus-like particle, and an antigen mixed with the
XX CC virus-like particle. The composition or the vaccine is useful in the
XX CC manufacture of a pharmaceutical for the treatment of a disorder or
XX CC disease such as allergies, tumours, chronic diseases and chronic viral
XX CC diseases. The composition is also useful for enhancing an immune response
XX CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
XX CC coat protein API protein subunit a virus like particle (VLP) that can be
XX CC used in the adjuvant of the invention.
XX SQ Sequence 329 AA;
Query Match 100.0%; Score 1749; DB 8; Length 329;
Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
1 MAKETVTLGNIGKQKOTLVNPRGVNPTNGVASTSQAGVPALEKRVTVSVSOPSRNR 60
61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRTLAALLASP 120
61 KNYKQVQKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDERAFVRTLAALLASP 120
121 LIIDAIDQINPQYWTLLIAGGSGSKPDVIPPDPIDPPGKGKTCFPAIWSLEEVYEP 180
121 LIIDAIDQINPQYWTLLIAGGSGSKPDVIPPDPIDPPGKGKTCFPAIWSLEEVYEP 180
181 PTKNRPWPIYNAVELOPREFDVALKDLGNTKMRWDSRLSTTTRGCGNGYIDLDAFY 240
181 PTKNRPWPIYNAVELOPREFDVALKDLGNTKMRWDSRLSTTTRGCGNGYIDLDAFY 240
241 LATDQAMBDQKYDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
241 LATDQAMBDQKYDIREGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300

Db 241 LATDQAMRDQKYDIRGKKPGAFGNIERIYLSINAYCSLSIDIAAYADGVIYGFMRDP 300
 QY 301 SSGGAIIPDFFTKCPICPIQAVIVPRA 329
 Db 301 SSGGAIIPDFFTKCPICPIQAVIVPRA 329

RESULT 8
 ADJ67147
 ID ADJ67147 standard; protein; 329 AA.
 AC ADJ67147;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Bacteriophage Qbeta coat protein for antigen display array.
 XX
 DE anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
 KM antigenic array.
 XX
 OS Bacteriophage Qbeta.
 XX
 PN WO2004009124-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007849.
 XX
 PR 19-JUL-2002; 2002US-0396638P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann MF, Fulurija A;
 XX
 DR WPI; 2004-132866/13.
 XX
 PT New composition comprising a core particle having a first attachment site
 PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
 PT peptide having a second attachment site, useful for treating obesity.
 PT
 PS Claim 12; SEQ ID NO 5; 175bp; English.
 XX
 CC The invention relates to a new composition comprising: (i) a core
 CC particle with at least one first attachment site; and (ii) at least one
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
 CC peptide, and where the second attachment site being consisting of an
 CC attachment site not naturally occurring with the antigen or antigenic
 CC determinant and an attachment site naturally occurring with the antigen
 CC or antigenic determinant, where the second attachment site is capable of
 CC association to the first attachment site, and where the ghrelin or a
 CC ghrelin peptide and the core particle interact through the association to
 CC form an ordered and repetitive antigen array. The composition is useful
 CC for treating obesity. The repetitive array may form part of a phage or
 CC bacterial display array. This peptide corresponds to a Bacteriophage
 CC Qbeta coat protein which can be used as part of the repetitive or antigenic
 CC array.
 CC
 XX
 SQ Sequence 329 AA;
 XX
 QY Query Match 100.0%; Score 1749; DB 8; Length 329;
 Db Best Local Similarity 100.0%; Pred. No. 3e-17;
 1 MAKLETVLAINIGKQKQTLVLRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRNR 60
 1 MAKLETVLAINIGKQKQTLVLRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRNR 60
 61 KNYVQVQKIONPRTACTANGSCDPSVTROAVADVFSTFOYSTDEERAFVRLAAILASP 120
 61 KNYVQVQKIONPRTACTANGSCDPSVTROAVADVFSTFOYSTDEERAFVRLAAILASP 120

QY 121 LLIDAIDQLNPAVYVTLTLIAGSGSGSKDPVTPDPPIPPPETGKTKCPFAWSLEVEYEP 180
 Db 121 LLIDAIDQLNPAVYVTLTLIAGSGSGSKDPVTPDPPIPPPETGKTKCPFAWSLEVEYEP 180
 QY 181 PTKRPMPIYNAVELQPREPVALKDLGNKWRDMSRLSYTFRRGGRNGYIDLDTATY 240
 Db 181 PTKRPMPIYNAVELQPREPVALKDLGNKWRDMSRLSYTFRRGGRNGYIDLDTATY 240
 QY 241 LATDQAMRDQKYDIRGKKPGAFGNIERIYLSINAYCSLSIDIAAYADGVIYGFMRDP 300
 Db 241 LATDQAMRDQKYDIRGKKPGAFGNIERIYLSINAYCSLSIDIAAYADGVIYGFMRDP 300
 QY 301 SSGGAIIPDFFTKCPICPIQAVIVPRA 329
 Db 301 SSGGAIIPDFFTKCPICPIQAVIVPRA 329

RESULT 9
 ADK52181
 ID ADK52181 standard; protein; 329 AA.
 AC ADK52181;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Bacteriophage Qbeta coat protein A1.
 XX
 DE neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
 KM core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
 KM coat protein; A1.
 XX
 OS Bacteriophage Qbeta.
 XX
 PN WO2004016282-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007864.
 XX
 PR 19-JUL-2002; 2002US-0396639P.
 XX
 PR 15-MAY-2003; 2003US-0470432P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PA (NOVS) NOVARTIS PHARMA AG.
 XX
 PI Bachmann MF, Tisot A, Ortmann R, Lueoend R, Staufenbiel M;
 PI Frey P;
 XX
 DR WPI; 2004-203731/19.
 XX
 PT Composition comprising a core particle with at least one attachment site,
 PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
 PT such as Alzheimer's disease.
 PT
 PS Claim 12; SEQ ID NO 5; 184bp; English.
 XX
 CC The invention describes a novel composition comprising a virus-like core
 CC particle with at least one attachment site, and an antigenic amyloid beta
 CC 1-6 peptide. The new composition comprises: a core particle with at least
 CC one first attachment site; and at least one antigen or antigenic
 CC determinant with at least one second attachment site, where the antigen
 CC or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
 CC second attachment site comprises: an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; or an attachment
 CC site naturally occurring with the antigen or antigenic determinant. The
 CC second attachment site is capable of association to the first attachment
 CC site and the beta 1-6 peptide and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC Alzheimer's disease and related diseases. This is the amino acid sequence
 CC of an RNA bacteriophage coat protein that can be used in the preparation
 CC of the compositions and vaccines of the invention.
 CC

SO Sequence 329 AA; 100.0%; Score 1749; DB 8; Length 329;
Query Match Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVSPSRNR 60
DB 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVSPSRNR 60
QY 61 KNYKVQVNIQNPACTANGSCDPSVTRQAVADVTSFYQYSTDEBRARVRETLAALLASP 120
DB 61 KNYKVQVNIQNPACTANGSCDPSVTRQAVADVTSFYQYSTDEBRARVRETLAALLASP 120
QY 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
DB 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
QY 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
DB 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
QY 181 PTKRNPMPPIYNAVELQPREFVALKDLIGNTKMRDWSRLSYTFRGCRNGYIDLDAITY 240
DB 181 PTKRNPMPPIYNAVELQPREFVALKDLIGNTKMRDWSRLSYTFRGCRNGYIDLDAITY 240
QY 241 LATQAMBDQKXDIREGKKPAGFNGIERFYLSKINAYCSLSDIAAYHADGVIVGFWMDP 300
DB 241 LATQAMBDQKXDIREGKKPAGFNGIERFYLSKINAYCSLSDIAAYHADGVIVGFWMDP 300
QY 301 SSGGAIIPDPFTKFDKTKCPIQAVIVPPRA 329
DB 301 SSGGAIIPDPFTKFDKTKCPIQAVIVPPRA 329

RESULT 10
ABR56440
ID ABR56440 standard; protein; 328 AA.
XX ABR56440;
AC ABR56440;
XX 23-OCT-2003 (revised)
DT 23-OCT-2003 (revised)
DT 23-OCT-2003 (first entry)
XX Bacteriophage Q-beta coat protein SEQ ID NO:11.
DE Bacteriophage Q-beta coat protein SEQ ID NO:11.
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KW cytosolic; virucide; antibacterial; antiparasitic; fungicide;
KW antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
KW antihydrolytic; antidiabetic; neuroprotective; nootropic; osteopathic;
KW antirheumatic; antidiabetic; vaccine; immunisation; infectious disease;
KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KW inflammatory autoimmune disease.
XX Bacteriophage Qbeta.
OS Bacteriophage Qbeta.
XX WO2003024480-A2.
XX 27-MAR-2003.
XX 16-SEP-2002; 2002WO-IB004252.
XX 14-SEP-2001; 2001US-0318967P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX Bachmann MF, Storm T, Lechner F;
XX WPI; 2003-363095/34.
XX A composition, useful for enhancing an immune response against an antigen
XX or immunising or treating tumors or infectious diseases, e.g. viral
XX infections.
XX

PS Disclosure; Page 168-169; 243pp; English.
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen. (C)
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytosolic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
CC antihydrolytic, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antirheumatic and antidiabetic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumours and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX

SO Sequence 328 AA; 99.1%; Score 1733.5; DB 6; Length 328;
Query Match Best Local Similarity 99.7%; Pred. No. 1.2e-169;
Matches 328; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVSPSRNR 60
DB 1 MAKETVTLGNIGKDGKQTLVLPNGVPTNGVSLSQAGVPALEKRVTVSVSPSRNR 60
QY 61 KNYKVQVNIQNPACTANGSCDPSVTRQAVADVTSFYQYSTDEBRARVRETLAALLASP 120
DB 61 KNYKVQVNIQNPACTANGSCDPSVTRQAVADVTSFYQYSTDEBRARVRETLAALLASP 120
QY 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
DB 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
QY 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
DB 121 LLIDAIDOLNPAWYWLTLIAGGSGSKPDPVIPPDPDPGKXTCPFAIWSLEVEYEP 180
QY 181 PTKRNPMPPIYNAVELQPREFVALKDLIGNTKMRDWSRLSYTFRGCRNGYIDLDAITY 240
DB 181 PTKRNPMPPIYNAVELQPREFVALKDLIGNTKMRDWSRLSYTFRGCRNGYIDLDAITY 240
QY 241 LATQAMBDQKXDIREGKKPAGFNGIERFYLSKINAYCSLSDIAAYHADGVIVGFWMDP 300
DB 241 LATQAMBDQKXDIREGKKPAGFNGIERFYLSKINAYCSLSDIAAYHADGVIVGFWMDP 300
QY 301 SSGGAIIPDPFTKFDKTKCPIQAVIVPPRA 329
DB 301 SSGGAIIPDPFTKFDKTKCPIQAVIVPPRA 329

RESULT 11
ABR44543
ID ABR44543 standard; protein; 328 AA.
XX ABR44543;
AC ABR44543;
XX 23-OCT-2003 (revised)
DT 23-OCT-2003 (revised)
DT 23-OCT-2003 (first entry)
XX Bacteriophage Q-beta coat protein SEQ ID NO:11.
DE Bacteriophage Q-beta coat protein SEQ ID NO:11.
XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
KW immunostimulant; cytosolic; antiallergic; virucide; antibacterial;
KW

KW immune response; immunisation; allergy; tumour; breast cancer;
 KM neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KM chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
 OS Bacteriophage Qbeta.
 PN WO2003024481-A2.
 XX
 PD 27-MAR-2003.
 PF 16-SEP-2002; 2002WO-IB004132.
 PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAUR/) MAURER P.
 PA (TISS/) TISSOT A.
 PA (SCHW/) SCHWARZ K.
 PA (MEIJ/) MEIJERINK E.
 PA (LIPD/) LIPOWSKY G.
 PA (PUMP/) PUMPENS P.
 PA (CIEL/) CIELENS I.
 PA (RENO/) RENHOFA R.
 XX
 PI Maurer P, Tisot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T;
 DR WPI; 2003-354564/33.
 XX
 PT New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX
 PS Disclosure; Page 247-249; 322pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
 CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention.
 CC (Updated on 23-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 328 AA:
 Query Match 99.1%; Score 1733.5; DB 6; Length 328;
 Best Local Similarity 99.7%; Pred. No. 1.2e-169; Indels 1; Gaps 1;
 Matches 328; Conservative 0; Mismatches 0;
 QY 1 MAKLEVTTLNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALERKRVTSVSOBSRNR 60
 DB 1 MAKLEVTTLNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALERKRVTSVSOBSRNR 60
 QY 61 KNYKVQVXIONPTACTANGSCDBSVTRQAVADVTFSTQYSTDERAFVTEILALASP 120

DB 61 KNYKVQVXIONPTACTANGSCDBSVTRQAVADVTFSTQYSTDERAFVTEILALASP 120
 QY 121 LLIDAIQDNLNAYMTLLIAGGSGSKDPVPVDPDPPIPPPGTGYTCEFAIWSLEVEYEP 180
 DB 121 LLIDAIQDNLNAYMTLLIAGGSGSKDPVPVDPDPPIPPPGTGYTCEFAIWSLEVEYEP 179
 QY 181 PTKRPMPIYNAVELQPREPDVALKDLIGNTKMDWDMSRLSYTFFRCGRNGYIDLDAITY 240
 DB 180 PTKRPMPIYNAVELQPREPDVALKDLIGNTKMDWDMSRLSYTFFRCGRNGYIDLDAITY 239
 QY 241 LATDQAMRDQKTDIREGKPGAFGNIRFYLKSLINAYCSLSDIAAAYADGVYIGFMRDP 300
 DB 240 LATDQAMRDQKTDIREGKPGAFGNIRFYLKSLINAYCSLSDIAAAYADGVYIGFMRDP 299
 QY 301 SSGAIPDPFTKPKDKCPIDQAVIVVPPRA 329
 DB 300 SSGAIPDPFTKPKDKCPIDQAVIVVPPRA 328
 RESULT 12
 ABR56445
 ID ABR56445 standard; protein; 329 AA.
 XX
 AC ABR56445;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Bacteriophage SP coat protein SEQ ID NO:16.
 XX
 KW Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
 KW antihypertoid; antidiabetic; neuroprotective; nootropic; osteopathic;
 KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 OS Bacteriophage SP.
 XX
 PN WO2003024480-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 16-SEP-2002; 2002WO-IB004252.
 XX
 PR 14-SEP-2001; 2001US-0318967P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann MF, Storni T, Lechner F;
 PI WPI; 2003-363095/34.
 XX
 DR WPI; 2003-363095/34.
 XX
 PT A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX
 PS Disclosure; Page 173-174; 243pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral

protection in an animal comprising introducing (C) into the animal. (C) has cytoskeletal, virocidic, antibacterial, antiparasitic, fungicidal, antiallergic, immunosuppressive, antidiabetic, antitumorigenic, antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic, antirheumatic and antirheumatic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunising or treating tumours and infectious diseases such as viral, bacterial, parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, drug addiction, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune diseases. ACC69838 to ACC69852 and ABR56401 to ABR56509 represent sequences used in the exemplification of the present invention

Sequence 329 AA;

Query Match 55.9%; Score 978; DB 6; Length 329;
Best Local Similarity 58.3%; Pred. No. 9.9e-92;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

2 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 61
1 AKLNVTLSTKIGKNDQTLTPRGVNPPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 60
62 NYKVOVKIQNPACTANGSCDPSVTRQAYADVTFFQYSTDEBRAVTELAALLASPL 121
61 NKVQIKIQNPACTCRD-ACDPSVTRSAFADVTLSYSTDEBRALITELAAALLADPL 119
122 LIDAIIDOLNPAYW-TLLIAGGSGSKPD---PVLPDPIDPPPGTKTCFPAIWSLEE 176
120 IVDADININPAMWALLVASSGGGNDPDPVPVVPD--VKPPDGTGRKCFACRYLGS 177
177 VYEPPTKRPWPIYNAVELQPREFDVALKDLGNTKMDWSRLS---YTFRRGGRNGY 233
178 IYEVGKESGP-DIYRGDEVSVTFDYALEDFGNTNMRWMDRLSDYDIANRRRCRNGY 236
234 IDLDATYIATDQAMRDQKDIRGKKPGAFGNIEFTYLSKSI--NAYCSLSDIAAYHADG 291
237 IDLDATAMQSDDFVLSGRGVAKVFPAGFSGIK---YILNITQGDAMLDLSEVTAYRSYG 293
292 VIVGFWRPDSSGGAIPDFTKDKTKCPIQAVIIVP 327
294 NVIGFWTD-SKSPQPLPTDFQNSANCPQVTIITP 328

RESULT 13

ABR44548 standard; protein; 329 AA.

ABR44548;

25-JUL-2003 (first entry)

Bacteriophage SP coat protein SEQ ID NO:16.

Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV, hepatitis B virus, lymphocytic choriomeningitis virus; vaccine; immunostimulant; cytotoxic; antiallergic; virocidic; antibacterial; immune response; immunisation; allergy; tumour; breast cancer; neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles; chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

Bacteriophage SP.

WO2003024481-A2.

27-MAR-2003.

16-SEP-2002; 2002WO-IB004132.

14-SEP-2001; 2001US-0318994P.
22-APR-2002; 2002US-0374145P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.
MAURER P.
TISSOT A.
SCHWAB K.
MEIJERINK E.
LITPOWSKY G.
PUMPENS P.
CIELENS I.
(RENH/) RENHOFER R.
Maurer P, Tissot A, Meijerink E, Litpowsky G, Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T; MPI; 2003-354564/33.

New compositions comprising immunostimulatory substances packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or viral infections.

Disclosure; Page 252-253; 322p; English.

The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an immunostimulatory substance. The immunostimulatory substance is bound to the VLP. Also described: (1) enhancing an immune response in an animal by introducing (C) into the animal; (2) producing (C) for enhancing an immune response in an animal; (3) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; and (4) immunising or treating an animal by: (a) administering the vaccine to the animal; (b) priming a T cell response in the animal by administering the vaccine; or (c) boosting a T cell response in the animal by administering the vaccine. (C) has immunostimulant, cytoskeletal, antiallergic, virocidic and antibacterial activities. (1) can be used in vaccines for enhancing an immune response in an animal, particularly a mammal or human. Specifically, (C) is useful for enhancing a B cell response, a T cell response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine comprising (C) can also be used for immunising or treating an animal, e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, reptiles or fish. (C) is particularly useful in prophylactic or therapeutic vaccines against allergies, tumors (e.g. breast cancers, neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis, measles or chicken pox), or bacterial infections (e.g. tuberculosis, pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44512 represent sequences used in the exemplification of the present invention

Sequence 329 AA;

Query Match 55.9%; Score 978; DB 6; Length 329;
Best Local Similarity 58.3%; Pred. No. 9.9e-92;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

2 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 61
1 AKLNVTLSTKIGKNDQTLTPRGVNPPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 60
62 NYKVOVKIQNPACTANGSCDPSVTRQAYADVTFFQYSTDEBRAVTELAALLASPL 121
61 NKVQIKIQNPACTCRD-ACDPSVTRSAFADVTLSYSTDEBRALITELAAALLADPL 119
122 LIDAIIDOLNPAYW-TLLIAGGSGSKPD---PVLPDPIDPPPGTKTCFPAIWSLEE 176
120 IVDADININPAMWALLVASSGGGNDPDPVPVVPD--VKPPDGTGRKCFACRYLGS 177
177 VYEPPTKRPWPIYNAVELQPREFDVALKDLGNTKMDWSRLS---YTFRRGGRNGY 233
178 IYEVGKESGP-DIYRGDEVSVTFDYALEDFGNTNMRWMDRLSDYDIANRRRCRNGY 236
234 IDLDATYIATDQAMRDQKDIRGKKPGAFGNIEFTYLSKSI--NAYCSLSDIAAYHADG 291
237 IDLDATAMQSDDFVLSGRGVAKVFPAGFSGIK---YILNITQGDAMLDLSEVTAYRSYG 293

QY 292 VIVGFWRDPSSGGAIPDPFTKFKDKCPICQAVIYVP 327
 DB 294 MWIGFWTD-SKSPQLPTDFTQNSANCPCVQYIIITP 328

RESULT 14

ID ADD24123 standard; protein; 329 AA.

AC ADD24123;

DE 15-JAN-2004 (first entry)

DE Bacteriophage SP coat protein A1.

XX vaccine composition; virus-like particle; core particle;
 XX first attachment site; antigen; antigenic determinant; prion protein;
 XX PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 XX Creutzfeldt-Jakob Disease; coat protein.

OS Bacteriophage SP.

PN WO2003059386-A2.

PD 24-JUL-2003.

PF 17-JAN-2003; 2003WO-EP000460.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 08-JUL-2002; 2002US-0393725P.

PR 18-JUL-2002; 2002US-0396590P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Maurer P, Pelliscio E, Renner WA;

XX WPI; 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phase) and at least one prion protein or peptide bound to the virus-like
 PT particle.

PS Disclosure; SEQ ID NO 16; 246bp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is the amino acid sequence of a coat
 CC protein from a bacteriophage which may be used during the creation of the
 CC vaccine composition of the invention.

XX Sequence 329 AA;

Query Match 55.9%; Score 978; DB 7; Length 329;

Best Local Similarity 58.3%; Pred. No. 9.9e-97; Indels 18; Gaps 9;

Matches 196; Conservative 45; Mismatches 77;

QY 2 AKLETVTLGNIGKDGKQTLVLRGVNPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 61

DB 1 AKLNQVTLRSKIGKNGDQTLVLRGVNPTNGVASLSQAGAVPALERKVTYSVSQPSNRK 60

QY 62 NYKVQVQIONPFACTANGSCDPSVTRQAVYADVTFSPFYQSTDERARAVRTELALLASPL 121

DB 61 NFKVQIKLQNPACTRD-ACDPVTRSAFADVTLSTFSYSTDERALLIRTELALLADPL 119

QY 122 LIDAIDQNPAYW-TLLIAGGSGSKPD----PIIPDPIDPPGKTKYTCPPAIWSLEE 176
 DB 120 IVDALDNLNPAVMALVAVSSGGGDNFEDPDVPVVPD--VKPDPGTGRYKCPFCACYRLGS 177

QY 177 VYBPPTKRPMPIYNAVELQREFVALKDLGNTKPRDMDSRLS---YTFPRGGRNGY 233

DB 178 IYEVKEGESP-DYERGGSESVTFDYALEDFLGNTMNRNWDQRLSDYDIANRRRCRGNGY 236

QY 234 IDLDATYATQAMWDOKYDIREGKPGAFGNIERFYLKSI--NAYCSLSDIAYHADG 291

DB 237 IDLDATYATQSDDFVLSGRYGRKRVKFPFGAFSGIK---YLNTIQGDAMLDSEVAYRBYG 293

QY 292 VIVGFWRDPSSGGAIPDPFTKFKDKCPICQAVIYVP 327

DB 294 MWIGFWTD-SKSPQLPTDFTQNSANCPCVQYIIITP 328

RESULT 15

ID ADJ82049 standard; protein; 329 AA.

AC ADJ82049;

DE 06-MAY-2004 (first entry)

DE Protein for RANKL antigen array to treat bone disease.

XX osteopathic; vaccine; core particle; antigenic determinant; RANKL;
 XX bone disease; encephalopathy; immune system stimulation.

OS Unidentified.

PN WO2003039225-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-EP012449.

PR 07-NOV-2001; 2001US-0331045P.

PR 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-1B000166.

PR 19-JUL-2002; 2002US-0396635P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-441430/41.

XX New compositions comprising a core particle and at least one antigen or
 PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
 PT of bone diseases, particularly mammalian encephalopathies.

PS Disclosure; SEQ ID NO 16; 222bp; English.

XX The invention relates to a composition comprising a core particle having
 CC at least one first attachment site, and at least one antigen or antigenic
 CC determinant having at least one second attachment site. The antigen or
 CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
 CC peptide. The second attachment site is (non-) naturally occurring with
 CC the antigen or antigenic determinant, and is capable of association to
 CC the first attachment site. The antigen or antigenic determinant and the
 CC core particle interact through the association to form an ordered and
 CC repetitive antigen array. The composition is useful as a medicament, or
 CC for the manufacture of a medicament for treating bone diseases. The
 CC composition is especially useful for as a vaccine for therapy or
 CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
 CC and for stimulating mammalian immune system. This sequence represents a
 CC protein of the invention.

XX Sequence 329 AA;

Query Match 55.9%; Score 978; DB 7; Length 329;
 Best Local Similarity 58.3%; Pred. No. 9.9e-92;
 Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY	2	AKLEVTYTLGNIGKDGKQTLVLPNGVNPNGVVASISQAGAVPALERKRVTVSVSOPSRNK	61
DB	1	AKLNQVTLISKIGKNGDQTLTLTPRGVNPNGVVASISQAGAVPALERKRVTVSVSOPSRNK	60
QY	62	NYKVQVKIQNPACTANGSCDPSVTRQAVADYTFSTOYSTDERAFVTELAALLASPL	121
DB	61	NFKVQIKIQNPACTARD-ACDPSVTRSAFADYTLSTSYSTDERALIRTELAALLADPL	119
QY	122	LIDALDQLPAYW-TLLINGGSGSKPD---PVLPDPIDPPPGTKYTCPPAIIWSLEE	176
DB	120	IYDAIDNINPAYMALLVASGSGGDNFSDPDVVPVVD--VKPPDGTGRYKCPFACYRLGS	177
QY	177	VVEPTKRNRPFIYNAVELQPREFDVALKDLGNTKWRDMSRLS---YTFRGCRNGY	233
DB	178	IYEVGKESGSP-DIERGDEVSVTFDYALBDPLGNTNWRWDQRLSDYDIANRRRCRNGY	236
QY	234	IDLDATYLATDQMRDQKYDIREGKKPGAFGNIERFIYLSI--NAYCSISDIAAYHADG	291
DB	237	IDLDATAMGSDDFVLSGRYGVKVKFPGAFSGIK---YLANIQDAMLDLSEVTAYRSYG	293
QY	292	VIVGFWRDPSGGAIPDFTKFDTKCPIQAVIIVP	327
DB	294	MVIGFWTD-SKSPQLPTDFTQFNSANCPQVYIITP	328

Search completed: January 4, 2005, 09:10:59
 Job time : 99.9054 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:05:21 ; Search time 25.8269 Seconds
(without alignments)
844.801 Million cell updates/sec

Title: US-10-622-064-4
Perfect score: 1749
Sequence: 1 MAKLETVLGNIGKDKQTL.....FTKPKTKCPQIVIVPRA 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/pdata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/pdata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/pdata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	5.5	1426	3	US-09-136-574A-43
2	95.5	5.5	1326	4	US-09-252-991A-17932
3	94	5.4	401	3	US-08-289-222E-3
4	94	5.4	401	2	US-09-054-526B-3
5	94	5.4	501	2	US-08-288-508C-2
6	94	5.4	501	4	US-08-981-490B-1
7	94	5.4	501	4	US-09-386-450D-2
8	91.5	5.2	920	4	US-09-463-402-6
9	91	5.2	1509	4	US-09-410-551B-23
10	91	5.2	1509	4	US-09-940-316B-23
11	90	5.1	495	1	US-08-455-559-10
12	90	5.1	495	3	US-09-145-060-10
13	90	5.1	495	3	PCT-US94-00657-10
14	90	5.1	1569	4	US-09-711-164-312
15	89.5	5.1	626	4	US-09-485-717-2
16	88.5	5.1	626	4	US-09-948-722-2
17	88.5	5.1	2972	3	US-09-579-181-2
18	88.5	5.1	3118	3	US-09-579-181-1
19	87	5.0	278	2	US-08-160-524A-4
20	87	5.0	283	2	US-08-160-524A-2
21	86.5	4.9	561	4	US-09-248-796A-18959
22	86	4.9	528	2	US-08-466-589-2
23	86	4.9	528	2	US-08-700-636-2
24	86	4.9	528	3	US-08-467-574-2
25	86	4.9	528	3	US-09-217-345-2
26	86	4.9	528	4	US-09-892-985-2
27	86	4.9	933	3	US-08-293-728-2

28	86	4.9	933	3	US-09-421-868-2	Sequence 2, Appl1
29	86	4.9	936	4	US-08-956-171E-5249	Sequence 5249, Ap
30	86	4.9	936	4	US-08-781-986A-5249	Sequence 5249, Ap
31	86	4.9	1651	3	US-09-540-245A-18	Sequence 18, Appl
32	85.5	4.9	312	1	US-08-414-625-2	Sequence 2, Appl1
33	84.5	4.8	1154	4	US-09-134-000C-6122	Sequence 6122, Ap
34	84	4.8	1469	4	US-09-262-537-58	Sequence 58, Appl
35	84	4.8	1577	2	US-08-793-824-2	Sequence 2, Appl1
36	83.5	4.8	415	4	US-09-252-991A-29602	Sequence 29602, A
37	82.5	4.7	695	1	US-08-164-839-8	Sequence 8, Appl1
38	82.5	4.7	695	1	US-08-583-799-8	Sequence 8, Appl1
39	82.5	4.7	696	1	US-08-164-839-10	Sequence 10, Appl
40	82.5	4.7	696	1	US-08-583-799-10	Sequence 10, Appl
41	82	4.7	148	4	US-09-270-767-42039	Sequence 42039, A
42	82	4.7	409	4	US-09-328-352-4249	Sequence 4249, Ap
43	82	4.7	842	4	US-08-591-502B-50	Sequence 50, Appl
44	82	4.7	842	4	US-08-591-502B-51	Sequence 51, Appl
45	82	4.7	982	4	US-09-556-877-176	Sequence 176, App

ALIGNMENTS

RESULT 1
US-09-136-574A-43
Sequence 43, Application US/09136574A
Patent No. 6294366
GENERAL INFORMATION:
APPLICANT: Farrington, Graham K.
Anderson, Paige
Gibbs, Moreland
Bergquist, Peter
Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for Treating Cellulose Containing Fabrics Using Truncated Cellulase Enzyme Compositions
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6294366
SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-09-136-574A-43

Query Match 5.5%; Score 97; DB 3; Length 1426;
Best Local Similarity 21.2%; Pred. No. 0.65;
Matches 80; Conservative 44; Mismatches 156; Indels 98; Gaps 20;

QY 22 LMRGVPNPNVNASLSQAG---AVPALERKRVTVSOPSRNRKVKYQVKNPACTA 77
DB 240 LSKRGV-PIHIGIQMOSHINVMPSVEINISIKLPSISIGIEIHITELMSLYN-YGSNE 297
QY 78 NGSCDPS--VTRQA--YADVTFSTQYS---TDEERAFVTELAALLAS-----PLTIDA 125
DB 298 NYSTPPQDLQRAQKXKDIETMLRKRYKGIYVCTVFWGKXDYSYMLNSSSKRDWPLFPD 357
QY 126 IQQLNPAVYTLTIAGSGSGSKDPVTPDPPIPP-----PRTGKRYTGP 168
DB 358 DYSAKPAVMSVLEAAGASAS-PSPTVTAPEPTPTPTVTAPEPTPTPTPTPTPTPTGS--- 412
QY 169 FAIWSLEEVYEPPTKN-----RPMPIYNAVELQPREPVALKDLGNTKMDW-- 216
DB 413 ---GKLVLY---KNNETSASTGSIKPM--FKIYVGGSSVD-----LSRYKIRYWT 456
QY 217 -DSRLSYTFRGCGRGYIDLDTATYATDQAMRDQKDIKREGKPGA----- 262
DB 457 VDDKQKQANCDMAQIGASVTFNFVKLSGSGVGAUYILEVFGSGAGLOPKDAGDIO 516
QY 263 -----FNIERTYIKSLINAYCSLSDIAYHADVIVGFM-RDPSGGAIPFDFT 311
DB 517 VRENKDMSNYNQADMSWLSMTIDYGENAKVLY-VDGVLV--WGOEP--GGATPAFPA 571
QY 312 KFDKTKCPIDAVIVPRA 329
DB 572 TATPTPTPTATVPTPTPA 589

RESULT 2

US-09-252-991A-17932
; Sequence 17932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17932
; LENGTH: 1326
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17932

Query Match 5.5%; Score 95.5; DB 4; Length 1326;
Best Local Similarity 24.9%; Pred. No. 0.84; Indels 105; Gaps 25;
Matches 92; Conservative 48; Mismatches 124;

QY 17 KQTLVLPNG---VNPTNGVASLSQAGAVPALEKRVTVSVOPSRNRKVKYQ-VKION 71
DB 338 EQQKIFQPRPKRKYVLSLN-VAEISL--TVGDIYVIDSGTARISRYAKVQRLPIEA 394
QY 72 PTACTAN-----GSCDPSVTRQAVADVTFSTQYSTEDEAFVTELAALLASPLI--- 122
DB 395 VSQASANQRKRCRVERGICVRLYSEDFNARPAFDPE--IRTNLAIVIIQMLRL 452
QY 123 --TADIDQANA-----YVTLI--IAGSGSGSKDPV---IDPPIDPPG----- 161
DB 453 GDIAFPPIEPDGAIKDGFLLQELISAVNREGOLPLGQRLRLPIDPLGMLLEAA 512

QY 162 -TGKTYCPFAIWSLEEVYEPPTKNRPMPIYNAVELQ-PREEDVALKULL--GNTKMDW 217
DB 513 QQG-----SLEEVLY-----TVASALSVDPRERPERVROQADQAHQWMDPD 554
QY 218 SRLS--YTFRFG-----CRGN--GYIDL-----DA-----TYLATDQAM-- 247
DB 555 SDFALINLMGFEORQALGSNALRSCNRFNLNLYLREWRRAHROLTLICRELKLPF 614
QY 248 -RDKYDIKREGK-KPGAFTNIERTF---YLSINAYCS--LSDIAYHADVIVG----- 295
DB 615 GRPAKAEKKEAKKAGASADNEREVPGLDYAAVHKALLISGLLSQIGKAEKGDYLGARQ 674
QY 296 -FWRDPSG 303
DB 675 RFWHPSSG 683

RESULT 3

US-08-289-222E-3
; Sequence 3, Application US/08289222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARNELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; CITY: SUITE 330
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-289-222E-3

Query Match 5.4%; Score 94; DB 3; Length 401;
Best Local Similarity 21.7%; Pred. No. 0.18;
Matches 77; Conservative 35; Mismatches 115; Indels 128; Gaps 18;

QY 22 LMPGVNPTNGVASLSQAGV-----ALEKRTVSVSQSR----- 58
DB 22 VTPKQLP--GGKAPPKAGSVSSFLKKAREPGPREPKEFRPPPTTPHEMYLSLYRT 79
QY 59 ---NRKVKYQVKIQNFPACTANGSCD-----PSYTRQAYV-DVTFSTQYSTDEER 106
DB 80 LSDADRKGNSSVKLEAGLANTITSFDKQDDRGPPVVRKQRYVPI-----SALEKD 132
QY 107 AFVETELALLASPLLDALDQNPAYWTLIAGG-----SGSKDPVPIPPPP 155
DB 133 GLGAEHLRLRKRP-----SDTAKPA-----APGGRAAQLKLSGSGRGPASLLDVRS 182
QY 156 IDPPPGTKYTCPPFINSLEBYEPTKQ-----RPWPLYNAVELOPREFDVALKD- 206
DB 183 VPGLDGSGMEV--FDIWLFRNF---KNSAQLCLELAWERGRAVDLRLGLGFDRAARQV 236
QY 207 -----LLGNTKWDMDWSRLSYTTFRGCGNGYIDLDT---YATPOAMBDQKYDIRE 256
DB 237 HEKALFLVFGRTKRD---LFFNEIKARSGOD---DKTYVEYLFSGRRKRRAPLATRQ 288
QY 257 GKKGPAFNIERFIYKLSINAYCSLS-----DIAYHADGV 292
DB 289 GKRPS-----KQLKARCSRKALHVNFKMGWMDWIIAPLEYEAFHCEGL 332

RESULT 4
US-09-054-526B-3
Sequence 3, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H TITEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: FOHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, MONICA CHIN
REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-3

Query Match 5.4%; Score 94; DB 3; Length 401;
Best Local Similarity 21.7%; Pred. No. 0.18;
Matches 77; Conservative 35; Mismatches 115; Indels 128; Gaps 18;

QY 22 LMPGVNPTNGVASLSQAGV-----ALEKRTVSVSQSR----- 58
DB 22 VTPKQLP--GGKAPPKAGSVSSFLKKAREPGPREPKEFRPPPTTPHEMYLSLYRT 79
QY 59 ---NRKVKYQVKIQNFPACTANGSCD-----PSYTRQAYV-DVTFSTQYSTDEER 106
DB 80 LSDADRKGNSSVKLEAGLANTITSFDKQDDRGPPVVRKQRYVPI-----SALEKD 132
QY 107 AFVETELALLASPLLDALDQNPAYWTLIAGG-----SGSKDPVPIPPPP 155
DB 133 GLGAEHLRLRKRP-----SDTAKPA-----APGGRAAQLKLSGSGRGPASLLDVRS 182
QY 156 IDPPPGTKYTCPPFINSLEBYEPTKQ-----RPWPLYNAVELOPREFDVALKD- 206
DB 183 VPGLDGSGMEV--FDIWLFRNF---KNSAQLCLELAWERGRAVDLRLGLGFDRAARQV 236
QY 207 -----LLGNTKWDMDWSRLSYTTFRGCGNGYIDLDT---YATPOAMBDQKYDIRE 256
DB 237 HEKALFLVFGRTKRD---LFFNEIKARSGOD---DKTYVEYLFSGRRKRRAPLATRQ 288
QY 257 GKKGPAFNIERFIYKLSINAYCSLS-----DIAYHADGV 292
DB 289 GKRPS-----KQLKARCSRKALHVNFKMGWMDWIIAPLEYEAFHCEGL 332

RESULT 5
US-08-288-508C-2
Sequence 2, Application US/08288508C
Patent No. 5994094
GENERAL INFORMATION:
APPLICANT: H titen, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
TITLE OF INVENTION: THE TGF- FAMILY
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marcelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,508C
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 26 829.3
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 18 222.8
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 20 157.5
FILING DATE: 09-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: JAHNS, Krietina M.
REGISTRATION NUMBER: P-41,092
REFERENCE/DOCKET NUMBER: P564-4019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-508C-2

Query Match 5.4%; Score 94; DB 2; Length 501;
Best Local Similarity 21.7%; Pred. No. 0.26; Mismatches 115; Indels 128; Gaps 18;
Matches 77; Conservative 35;

QY 22 LNPRGVNPTNGVASISQAGAVP-----ALEKRVTVSVSQPSR----- 58
DB 122 VTPKQGLP--GGKAPPKAGSVSSFLKKAREGPPREPKERPPRPPIPHHEMYMLSLYRT 179
QY 59 ---NRKNKYQVQKIQNPACTANGSCD-----PSYTRQAYV-DVTFSTFOYSTDEER 106
DB 180 LSDADRKGGNSSVKLEAGLANITTSFIDKGQDRGVVAKRQYVFDI-----SALEKD 232
QY 107 AFVTEELALLASPLILDAIDQNPAYWTLTLAGG-----SGSKDPVYIDPP 155
DB 233 GLIGABELRLIRKKP-----SDTAKPA-----APGGRAAQLKSSCPSGRQPSLIDVRS 282
QY 156 IDPPPTGKYTCPPFAIWSLEEVYEPPPTKN-----RPMPIYNAVELQPREFDVALKD- 206
DB 283 VGLDGSQGEV--FQIWKLFRRNF-----KNSAQCLELAMEGRVADLGLGFDRAARQV 336
QY 207 -----LIGNTYKRWDMDSRLSTYTPRCGRNGYIDLDT--YATDQAMPDQKTDIRE 256
DB 337 HEKALFLVFGRTKRD-----LFFNEIKARSGQD--DQIVVEYLFQRRKRRAPLATQ 388
QY 257 GKKGAFGNIERTYIKSINAYCSLS-----DIAAYHADGV 292
DB 389 GKRRPS-----KNLKARCSKRALHVNFKDMGMDMTIAPLEYEAFHCEGL 432

RESULT 6

US-08-981-490B-1
Sequence 1, Application US/08981490B
Patent No. 6531450
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B
CURRENT FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE/195 25 416.3
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 501
TYPE: PRT

ORGANISM: Homo sapiens
US-08-981-490B-1

Query Match 5.4%; Score 94; DB 4; Length 501;
Best Local Similarity 21.7%; Pred. No. 0.26; Mismatches 115; Indels 128; Gaps 18;
Matches 77; Conservative 35;

QY 22 LNPRGVNPTNGVASISQAGAVP-----ALEKRVTVSVSQPSR----- 58
DB 122 VTPKQGLP--GGKAPPKAGSVSSFLKKAREGPPREPKERPPRPPIPHHEMYMLSLYRT 179
QY 59 ---NRKNKYQVQKIQNPACTANGSCD-----PSYTRQAYV-DVTFSTFOYSTDEER 106
DB 180 LSDADRKGGNSSVKLEAGLANITTSFIDKGQDRGVVAKRQYVFDI-----SALEKD 232
QY 107 AFVTEELALLASPLILDAIDQNPAYWTLTLAGG-----SGSKDPVYIDPP 155
DB 233 GLIGABELRLIRKKP-----SDTAKPA-----APGGRAAQLKSSCPSGRQPSLIDVRS 282
QY 156 IDPPPTGKYTCPPFAIWSLEEVYEPPPTKN-----RPMPIYNAVELQPREFDVALKD- 206
DB 283 VGLDGSQGEV--FQIWKLFRRNF-----KNSAQCLELAMEGRVADLGLGFDRAARQV 336
QY 207 -----LIGNTYKRWDMDSRLSTYTPRCGRNGYIDLDT--YATDQAMPDQKTDIRE 256
DB 337 HEKALFLVFGRTKRD-----LFFNEIKARSGQD--DQIVVEYLFQRRKRRAPLATQ 388
QY 257 GKKGAFGNIERTYIKSINAYCSLS-----DIAAYHADGV 292
DB 389 GKRRPS-----KNLKARCSKRALHVNFKDMGMDMTIAPLEYEAFHCEGL 432

RESULT 7

US-09-386-450D-2
Sequence 2, Application US/09386450D
Patent No. 6764994
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TGF-? Family
FILE REFERENCE: 100564-09022
CURRENT APPLICATION NUMBER: US/09/386,450D
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: US 08/288,508
PRIOR FILING DATE: 1994-08-10
PRIOR APPLICATION NUMBER: DE P 43 26 829.3
PRIOR FILING DATE: 1993-08-10
PRIOR APPLICATION NUMBER: DE P 44 18 222.8
PRIOR FILING DATE: 1994-05-25
PRIOR APPLICATION NUMBER: DE P 44 20 157.5
PRIOR FILING DATE: 1994-06-09
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(501)
OTHER INFORMATION: TGF-beta protein MP-52 precursor
US-09-386-450D-2

Query Match 5.4%; Score 94; DB 4; Length 501;
Best Local Similarity 21.7%; Pred. No. 0.26; Mismatches 115; Indels 128; Gaps 18;
Matches 77; Conservative 35;

QY 22 LNPRGVNPTNGVASISQAGAVP-----ALEKRVTVSVSQPSR----- 58
DB 122 VTPKQGLP--GGKAPPKAGSVSSFLKKAREGPPREPKERPPRPPIPHHEMYMLSLYRT 179
QY 59 ---NRKNKYQVQKIQNPACTANGSCD-----PSYTRQAYV-DVTFSTFOYSTDEER 106

Db 180 LSDADRGKGNSSVGLAGLANTITTSFDGQDDRGVVKRQVFI-----SLEKD 232
Qy 107 AFVTEALALLASPLLIDAIIDOLNPAWTLIAGG-----SSKDPDPVIPP 155
Db 233 GLGAEFLRLRKPP-----SDTAKPA-----APGGRAQLKSSGSPGRQPSLIDVVS 282
Qy 156 IDPPGTGKYTCPPAIVSLSEVEEYPTKQ-----RPMPIYNAVELOPREVDALKD- 206
Db 283 VGLDGSQWVEV--FDIWKLFRRNF-----KNSAQCLTELAMERGRAVDLRLGFDRAARQV 336
Qy 207 -----LLGNTKRWDMDSRLSYTTRGCGNGYIDLDT--YLATDQAMDQKDIIE 256
Db 337 HEKALFLVFGRTKKD-----LFENELKARSQD--DITYEYELFSQRRKRAPLATQ 388
Qy 257 GKGPAGFNGIERFIYLSINAYCSLS-----DIAAYHADGV 292
Db 389 GKRP-----KNLKARCSRALHVNFRKMGMDMIAPLEYEAFHCEGL 432

RESULT 8

US-09-463-402-6
Sequence 6, Application US/09463402
Patent No. 6586510

GENERAL INFORMATION:
APPLICANT: Lubitz, Werner
APPLICANT: Resch, Stephanie
TITLE OF INVENTION: Secretion of Carrier-bound Proteins into the Periplasm
TITLE OF INVENTION: and into the Extracellular Space
FILE REFERENCE: 05649059
CURRENT APPLICATION NUMBER: US/09/463,402
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: DE19732829.6
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: PCT/EP98/04723
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 920
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-463-402-6

Query Match 5.2%; Score 91.5; DB 4; Length 920;
Best Local Similarity 21.5%; Pred. No. 1.3;
Matches 64; Conservative 40; Mismatches 87; Indels 107; Gaps 15;

Qy 55 QPSNRKRYKQVKIQNPTACTANGSCDPSVTRQAYADYTFSF----- 97
Db 4 QPKSYRK-----FVATTATTAAMVAVASAVVSAASFTDVAPOYKALIDVLSTGATKGT 58
Qy 98 -TQYTDERRAVRTEBLALLASPLLIDAIIDOLNPAWTL-----LLIAGGSG 144
Db 59 ETKFGEYDE--TTRIDAAVILARVKTLD--VDNAKAGFDVPRAKYVNAIVEGAVLNG 115
Qy 145 SKPDVIPPDPIDPPGTGKYTCPPAIVSLSEVEEYPTKQRPMPYNAVELOPREVDAL 204
Db 116 KAP-----GKF-----GAYDPLR-----VEM-----A 133
Qy 205 KDLGNTKRWDMDSRLSYTTRGCGNGYIDLDTATDQAMDQKDIIEGKPP--G 261
Db 134 KIARRYKLKADVDLKLPT-----DVNDTWAPVYKAL--YKYEVTGKPTPSFG 180
Qy 262 AFGNIER-----FIY-LKSINAYCSLSIAAHADGVYGFPRDSSGGAIFPDITKF 313
Db 181 AYQNTTRGDFQAFVYRAVINAVPEIVEYAVNSTVKTTF-----NTQIADVDPTNF 233

RESULT 9
US-09-410-551B-23
Sequence 23, Application US/09410551B
Patent No. 6503737

GENERAL INFORMATION:
APPLICANT: KOSAN BIOSCIENCES, Inc.
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL

APPLICANT: WU, KAI
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20026.00
CURRENT APPLICATION NUMBER: US/09/410,551B
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/102,748
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1509
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
US-09-410-551B-23

Query Match 5.2%; Score 91; DB 4; Length 1509;
Best Local Similarity 19.9%; Pred. No. 3.2;
Matches 37; Conservative 35; Mismatches 70; Indels 44; Gaps 6;

Qy 9 LGNICKDGKQTLVLPNG-----VNPNGVASLSQAGVPALEKRV----- 49
Db 501 VSSFGVSGTNAHVILAGEVETETTPAASPSGDLPLVASRPPALDQIRRLRAYIDTTPD 560
Qy 50 --TVESVQPSNRKRYKQVKIQNPTACT-----ANGSCPSTVTRQAYAD 92
Db 561 VDRVAVAQTLARHTFARAVALLGDTVITTPADRPDELVPYSSGQTHPAMGQ-LAD 619
Qy 93 VTFSTQYSTD--ERRAFVTEALALLASPLLIDAIIDOLNPAWTLIA---GGGSGS 145
Db 620 SSVFPAERMAECALREFVDWDLFTVLDDPAVDVAVVCPASWAMVSLAAVWQAAQGV 679
Qy 146 KDPYI 151
Db 680 RPDYI 685

RESULT 10
US-09-940-316B-23
Sequence 23, Application US/09940316B
Patent No. 6759536
GENERAL INFORMATION:
APPLICANT: KOSAN BIOSCIENCES, Inc.
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL
TITLE OF INVENTION: POLYKETIDES ENCODING THE FKbA GENE OF THE FK-520 POLYKETIDE SYNTHASE
TITLE OF INVENTION: GENE CLUSTER
FILE REFERENCE: 30062-20026.11
CURRENT APPLICATION NUMBER: US/09/940,316B
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/410,551
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/102,748

PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1509
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
US-09-940-316B-23

Query Match 5.2%; Score 91; DB 4; Length 1509;
Best Local Similarity 19.9%; Pred. No. 3.2;
Matches 37; Conservative 35; Mismatches 70; Indels 44; Gaps 6;

QY 9 LGNIGKDGKQTLVNLNRG-----VNPTNGVASLSQAGAVPLERKRV----- 49
DB 501 VSSFGVSGTNAHVILAGPVTETPPASPSGDLPLVSARSPEALDQIRRLRAYLDTTPD 560
QY 50 --TVSSQPSRRKKNKQVKNPTACT-----ANGSCDPSVTRQAVAD 92
DB 561 VDRVAQAQTLARTHTAHRAVLIGDTVITPPADRPDELVFVYSGGTGHPAWGEO-LAD 619
QY 93 VTFSTQVSTD--ERRAFVTEALALASPLIDAIQINPAVYTLIA--GGSGS 145
DB 620 SSVVFERRMAECALAREFVMDLFTVLDPAVVDVQVQPSAMWMTSLAAVWQAGV 679
QY 146 KDDPVT 151
DB 680 RPDVAVI 685

RESULT 11
US-08-455-559-10
Sequence 10, Application US/08455559
Patent No. 5801014
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-455-559-10

Query Match 5.1%; Score 90; DB 1; Length 495;
Best Local Similarity 22.0%; Pred. No. 0.71;
Matches 77; Conservative 39; Mismatches 116; Indels 118; Gaps 18;

QY 22 INPRGVNPTNGVASLSQAGAVPA-----LEKRVTSVSOPSR----- 58
DB 116 VTPKQGLP-GKAS-SKASAPSSFLTKTRPPTPRPEKPEFPPIPTPHEVLSLYRT 173
QY 59 ---NRKATKQVKNQNPACTANGSCD-----PSVTRQAYA-DVTFSTQVSTDEER 106
DB 174 LSDARKKGNSSVKLEAGLANTITSFTIKGQDDRGPAVRKQTVFDI-----SALEKD 226
QY 107 AVFRTALALASPLIDAIQINPAVYTLIAAGSGSGKPPVPIPPIDPP 160
DB 227 GLGAEHLRLRKPL-----DVAKPAVPSGSGVAQKLSSCSGQPAALLDVRSVPGLD 281
QY 161 GTGKYTCPPAIVSLSEVEYEPPTKN-----RPWPIYNAVELQPEF-----DVAL 204
DB 282 GSGWEV--FDIKLFRNF-----KNSAQCLLEAWERGRAVDLRGLGFERTARQVHEKAL 335
QY 205 KOLLGNTKRWDSRLSTTFRCGNGYIIDAT---YLADQAMROKVIIRGSKRG 261
DB 336 FLVFGTKKRD---LFENEIRARSGOD---DKTYEYLFQRRRRRAPLANRQSKRS 387
QY 262 AFGNTERFYLKINAYCSLS-----DIAAYHADGV 292
DB 388 -----KXLRKRCRKALHVNFKDMGMDWMIAPLEYEAHFCEGL 426

RESULT 12
US-09-145-060-10
Sequence 10, Application US/09145060
Patent No. 6245896
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
US-09-145-060-10

Query Match 5.1%; Score 90; DB 3; Length 495;
Best Local Similarity 22.0%; Pred. No. 0.71;
Matches 77; Conservative 39; Mismatches 116; Indels 118; Gaps 18;

22 INPGRVPTNGVASLSQAGAVPA-----LEKRVTSVQSPSR----- 58
116 VTPKQQLP-GGKAS-SKASGAPSSFLKKTRPGTPRREKPEFRPPPTTTPHEMYLSYRT 173
59 -----NRKYKQVQKIQNPACTANGSCD-----PSYTRQAYA-DYTFSTQYSTDEER 106
174 LSDADRKGNSSVKLEAGLANITTSFIDKGDDBPAVKQRYVFDI-----SALEKD 226
107 AFVTELAALLASPLLIDALIDNPAYWT-----LLIAGGSGSKPDVIVDPPIIDPP 160
227 GLLGAEHLIRKKPL-----DVAKPAVPSGSRVAQLKSSCPGQOPALLDVRSPGLD 281
161 GTGKYTCFPAIWSLEVEVEPTKN-----RPWPIYNAVELQPREF-----DVAL 204
282 GSGWEV--FDIWKLP--KNSAQLCLELAEAMERGRAVDLRGLGFERTARQVHEKRL 335
205 KDLGNTKWRDMSRLSYTFRGCRNGYIDLAT--YLATDQMRDQKYDIRGKKPG 261
336 FLVFGRTKKRD--LFNEIKARSGOD--DKTVYEYLFQRRKRRAPIANROGKRPS 387
262 AFGNIERTIYKSIAYCSLS-----DIAAYHAGCV 292
388 -----KNLKARCSRKALHVNFKDMGMDWMIAPLEYEAHCGL 426

RESULT 13

PCT-US94-00657-10.
Sequence 10, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELEPHONE: 619/445-5100
TELEFAX: 619/445-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
PCT-US94-00657-10

Query Match 5.1%; Score 90; DB 5; Length 495;

Best Local Similarity 22.0%; Pred. No. 0.71;
Matches 77; Conservative 39; Mismatches 116; Indels 118; Gaps 18;

22 INPGRVPTNGVASLSQAGAVPA-----LEKRVTSVQSPSR----- 58
116 VTPKQQLP-GGKAS-SKASGAPSSFLKKTRPGTPRREKPEFRPPPTTTPHEMYLSYRT 173
59 -----NRKYKQVQKIQNPACTANGSCD-----PSYTRQAYA-DYTFSTQYSTDEER 106
174 LSDADRKGNSSVKLEAGLANITTSFIDKGDDBPAVKQRYVFDI-----SALEKD 226
107 AFVTELAALLASPLLIDALIDNPAYWT-----LLIAGGSGSKPDVIVDPPIIDPP 160
227 GLLGAEHLIRKKPL-----DVAKPAVPSGSRVAQLKSSCPGQOPALLDVRSPGLD 281
161 GTGKYTCFPAIWSLEVEVEPTKN-----RPWPIYNAVELQPREF-----DVAL 204
282 GSGWEV--FDIWKLP--KNSAQLCLELAEAMERGRAVDLRGLGFERTARQVHEKRL 335
205 KDLGNTKWRDMSRLSYTFRGCRNGYIDLAT--YLATDQMRDQKYDIRGKKPG 261
336 FLVFGRTKKRD--LFNEIKARSGOD--DKTVYEYLFQRRKRRAPIANROGKRPS 387
262 AFGNIERTIYKSIAYCSLS-----DIAAYHAGCV 292
388 -----KNLKARCSRKALHVNFKDMGMDWMIAPLEYEAHCGL 426

RESULT 14

US-09-711-164-312
Sequence 312, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Chisen, Kari
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 312
LENGTH: 1569
TYPE: PRT
ORGANISM: Escherichia coli
US-09-711-164-312

Query Match 5.1%; Score 90; DB 4; Length 1569;
Best Local Similarity 20.4%; Pred. No. 4.5; Indels 142; Gaps 18;
Matches 81; Conservative 32; Mismatches 143;

6 TTTLGNIGKDGKQTLVLPNG--VNPTNGVASLSQAGAVPALEKRVTSVQSPSRNRKN 62
1060 TLTGNGVDTTLADLTAAISRGVWLNNSNCSAGTNC-----EYRVN-----SLAND 1107
63 YKQVQKIQNPACTANGSCDPSYTRQAYADYTFSTQYSTDEERAFVTELAALLASPL 122
1108 GDVYLSAQTAAPATNGVYNTLTNELSGSNF-----YLTHTNAGSGDQLV 1155
123 ID-----AIDQNPAYWTLLIAGGSGS----- 145
1156 VNNATNGPKIFVQDTGVSPOSDDAMTLVKTGGASLTGNTGTFVULGITYEYLSKDG 1215
146 -----KDPV--IPDPIDPPGTGKYTCFPAIWSLEVEVEPTKNRPP-- 188
1216 NSNNWLTNDVKNPPIPNPKRDPKDPKDPNPKPD-----TPDPTLPVPEKRTPTST 1271
189 --IYNAVELQPREFVALKDL-----GNTKRDMSRLSYTFRGCRNGYID 235
1272 AAVLNMAATLPLVFDALNSIRERLINIMKASPHNNVW-----GATYNT-----RNNVTTD 1322

[illegible]

RESULT 15
US-09-485

```

Sequence 2 Application US/09485717
Patent No. 6673353
GENERAL INFORMATION:
APPLICANT: Kauffmann, Stefan
APPLICANT: Hees, Jrgen
TITLE OF INVENTION: Tuberculosis Vaccine
FILE REFERENCE: 16862PUS
CURRENT APPLICATION NUMBER: US/09/485, 717
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: EP 97114614. 7
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PCT/EP98-05109
PRIOR FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2

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Query Match	5.1%;	Score	89.5;	DB	4;	Length	626;
Best Local Similarity	23.5%;	Pred	No.1.2;				
Matches	31;	Conservative	23;	Mismatches	43;	Indels	35;
				Gaps		5;	

QY 50 TVSVSQPSRRNKRYKQVYKIQNPFTACIANGSCDSPVTR-----QAADVTSPFTQYST 103

Db 198 TLTSIDPFGMTQDNKIYVK--NATKSNVNNNAVNTLVRRMNEKQAQAAPNVS---AKIDYD 252

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QY      104 EERAFV RTEIAA 115
         :| | : :| |
Db      253 DEMAYSESQLIA 264
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Search completed: January 4, 2005, 09:35:42
Job time : 27.8269 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 81.5897 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-4

Perfect score: 1749
Sequence: 1 MAKETVTNLGNIGKDGKQTL.....FTKFKTKPCIPQAVIVPRA 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US61_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US61_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1749	100.0	329	14	US-10-289-454-11 Sequence 11, Appl
2	1749	100.0	329	14	US-10-050-902-217 Sequence 217, App
3	1749	100.0	329	14	US-10-050-898-217 Sequence 217, App
4	1749	100.0	329	14	US-10-346-190-11 Sequence 11, Appl
5	1749	100.0	329	15	US-10-465-811-2 Sequence 11, Appl
6	1749	100.0	329	15	US-10-289-456-11 Sequence 11, Appl
7	1749	100.0	329	15	US-10-622-064-4 Sequence 4, Appl
8	1749	100.0	329	15	US-10-622-124-5 Sequence 5, Appl
9	1749	100.0	329	16	US-10-622-087-5 Sequence 5, Appl
10	1733.5	99.1	328	14	US-10-243-739-11 Sequence 11, Appl
11	1733.5	99.1	328	14	US-10-244-065-11 Sequence 11, Appl
12	978	55.9	329	14	US-10-243-739-16 Sequence 16, Appl
13	978	55.9	329	14	US-10-244-065-16 Sequence 16, Appl

14	978	55.9	329	14	US-10-289-454-16	Sequence 16, Appl
15	978	55.9	329	14	US-10-346-190-16	Sequence 16, Appl
16	978	55.9	329	15	US-10-465-811-7	Sequence 7, Appl
17	978	55.9	329	15	US-10-289-456-16	Sequence 16, Appl
18	978	55.9	329	15	US-10-622-064-28	Sequence 28, Appl
19	978	55.9	329	15	US-10-622-124-10	Sequence 10, Appl
20	978	55.9	329	15	US-10-622-087-10	Sequence 10, Appl
21	978	55.9	330	14	US-10-050-902-254	Sequence 254, App
22	978	55.9	330	14	US-10-050-898-254	Sequence 254, App
23	897.5	51.3	330	14	US-10-243-739-20	Sequence 20, Appl
24	897.5	51.3	330	14	US-10-244-065-20	Sequence 20, Appl
25	897.5	51.3	330	14	US-10-289-454-20	Sequence 20, Appl
26	897.5	51.3	330	14	US-10-050-902-167	Sequence 167, App
27	897.5	51.3	330	14	US-10-050-898-167	Sequence 167, App
28	897.5	51.3	330	14	US-10-346-190-20	Sequence 20, Appl
29	897.5	51.3	330	15	US-10-465-811-11	Sequence 11, Appl
30	897.5	51.3	330	15	US-10-289-456-20	Sequence 20, Appl
31	897.5	51.3	330	15	US-10-622-064-32	Sequence 32, Appl
32	897.5	51.3	330	15	US-10-622-124-14	Sequence 14, Appl
33	897.5	51.3	330	16	US-10-622-087-14	Sequence 14, Appl
34	663	37.9	132	14	US-10-243-739-10	Sequence 10, Appl
35	663	37.9	132	14	US-10-244-065-10	Sequence 10, Appl
36	663	37.9	132	14	US-10-289-454-10	Sequence 10, Appl
37	663	37.9	132	14	US-10-050-902-159	Sequence 159, App
38	663	37.9	132	14	US-10-050-898-159	Sequence 159, App
39	663	37.9	132	14	US-10-346-190-10	Sequence 10, Appl
40	663	37.9	132	15	US-10-465-811-1	Sequence 1, Appl
41	663	37.9	132	15	US-10-289-456-10	Sequence 10, Appl
42	663	37.9	132	15	US-10-622-064-3	Sequence 3, Appl
43	663	37.9	132	15	US-10-622-124-4	Sequence 4, Appl
44	663	37.9	132	16	US-10-622-087-4	Sequence 4, Appl
45	655	37.4	132	14	US-10-243-739-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-289-454-11
Sequence 11, Application US/10289454
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Bachmann, Gary
APPLICANT: Sonderegger, Ivo
TITLE OR INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT FILING DATE: 2003-02-10
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
LENGTH: 329
TYPE: PRT
ORGANISM: Bacteriophage Q-beta CP
US-10-289-454-11
Query Match 100.0%; Score 1749; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTNLGNIGKDGKQTLVLPNGVNPPTGVSALSDGAVPALEKRVTVSVSPSRNR 60
DB 1 MAKETVTNLGNIGKDGKQTLVLPNGVNPPTGVSALSDGAVPALEKRVTVSVSPSRNR 60

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QY 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDDEBAFVTELAALLASP 120
DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDDEBAFVTELAALLASP 120
QY 121 L1IDAIDQINPAWYTLIIAGGSGSKPDPIPPIDPPGKGKTCPPAIIWSLEEVYEP 180
DB 121 L1IDAIDQINPAWYTLIIAGGSGSKPDPIPPIDPPGKGKTCPPAIIWSLEEVYEP 180
QY 181 PTKNRWPPIYNNAVELOPREFDVALKDLGNTKMRDMSRLSTYTFRGCRGNGYIIDDATY 240
DB 181 PTKNRWPPIYNNAVELOPREFDVALKDLGNTKMRDMSRLSTYTFRGCRGNGYIIDDATY 240
QY 241 LATDQMRDQKDIIEGKKPGAFGNIERTIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
DB 241 LATDQMRDQKDIIEGKKPGAFGNIERTIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329

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RESULT 2

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US-10-050-902-217
; Sequence 217, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisoc, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Plosek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 217
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-050-902-217

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Query Match 100.0%; Score 1749; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 3,8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRNR 60
DB 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRNR 60
QY 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDDEBAFVTELAALLASP 120
DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDDEBAFVTELAALLASP 120
QY 121 L1IDAIDQINPAWYTLIIAGGSGSKPDPIPPIDPPGKGKTCPPAIIWSLEEVYEP 180
DB 121 L1IDAIDQINPAWYTLIIAGGSGSKPDPIPPIDPPGKGKTCPPAIIWSLEEVYEP 180
QY 181 PTKNRWPPIYNNAVELOPREFDVALKDLGNTKMRDMSRLSTYTFRGCRGNGYIIDDATY 240
DB 181 PTKNRWPPIYNNAVELOPREFDVALKDLGNTKMRDMSRLSTYTFRGCRGNGYIIDDATY 240

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QY 241 LATDQMRDQKDIIEGKKPGAFGNIERTIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
DB 241 LATDQMRDQKDIIEGKKPGAFGNIERTIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329

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RESULT 3

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US-10-050-898-217
; Sequence 217, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisoc, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Plosek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staudenfel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 217
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-050-898-217

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Query Match 100.0%; Score 1749; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 3,8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRNR 60
DB 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRNR 60
QY 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDDEBAFVTELAALLASP 120
DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDDEBAFVTELAALLASP 120
QY 121 L1IDAIDQINPAWYTLIIAGGSGSKPDPIPPIDPPGKGKTCPPAIIWSLEEVYEP 180
DB 121 L1IDAIDQINPAWYTLIIAGGSGSKPDPIPPIDPPGKGKTCPPAIIWSLEEVYEP 180
QY 181 PTKNRWPPIYNNAVELOPREFDVALKDLGNTKMRDMSRLSTYTFRGCRGNGYIIDDATY 240
DB 181 PTKNRWPPIYNNAVELOPREFDVALKDLGNTKMRDMSRLSTYTFRGCRGNGYIIDDATY 240
QY 241 LATDQMRDQKDIIEGKKPGAFGNIERTIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
DB 241 LATDQMRDQKDIIEGKKPGAFGNIERTIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTEKDKTCPIQAVIVPRA 329

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RESULT 4

US-10-346-190-11
 ; Sequence 11, Application US/10346190
 ; Publication No. US20030219459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Pelliccioli, Erica
 ; APPLICANT: Renner, Wolfgang A.
 ; TITLE OF INVENTION: Protein Carrier-Conjugates
 ; FILE REFERENCE: 1700.0290003
 ; CURRENT APPLICATION NUMBER: US/10/346,190
 ; CURRENT FILING DATE: 2003-01-17
 ; PRIOR APPLICATION NUMBER: 60/396,590
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/393,725
 ; PRIOR FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: PCT/IB02/00166
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: 10/050,902
 ; PRIOR FILING DATE: 2002-01-18
 ; NUMBER OF SEQ ID NOS: 164
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage Q-beta
 US-10-346-190-11

Query Match 100.0%; Score 1749; DB 14; Length 329;
 Best Local Similarity 100.0%; Pred. No. 3.8e-161;
 Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTGNGKDGKQTLVNPGRVPTNGVSLQAGVPALEKRVTVSVQPSRRR 60
 DB 1 MAKETVTGNGKDGKQTLVNPGRVPTNGVSLQAGVPALEKRVTVSVQPSRRR 60
 QY 61 KKKYQVKIQNPTACTANGSCDPSVTROAYADVTSFTQYSTDERAFVRTLAALLASP 120
 DB 61 KKKYQVKIQNPTACTANGSCDPSVTROAYADVTSFTQYSTDERAFVRTLAALLASP 120
 QY 121 LIIDAIIDQNPAYWTLILAGGSGSKPDVIPPDPIDPPGIGKTCPPAIIWSLEEVYP 180
 DB 121 LIIDAIIDQNPAYWTLILAGGSGSKPDVIPPDPIDPPGIGKTCPPAIIWSLEEVYP 180
 QY 181 PTKNRPPIYNAVELQPREFDVALKDLGNTKMRDWSLSYTPRGCRNGYIDDATY 240
 DB 181 PTKNRPPIYNAVELQPREFDVALKDLGNTKMRDWSLSYTPRGCRNGYIDDATY 240
 QY 241 LATDQMRDQKDIIEGKKPGAFGNIERIYIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
 DB 241 LATDQMRDQKDIIEGKKPGAFGNIERIYIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
 QY 301 SSGGAIIPDFTKEDTKCPICQAVIYVPPRA 329
 DB 301 SSGGAIIPDFTKEDTKCPICQAVIYVPPRA 329

RESULT 5

US-10-465-811-2
 ; Sequence 2, Application US/10465811
 ; Publication No. US20040005338A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BACHMANN, MARTIN F
 ; APPLICANT: RENNER, WOLFGANG A
 ; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
 ; FILE REFERENCE: 1700.0290004
 ; CURRENT APPLICATION NUMBER: US/10/465,811
 ; CURRENT FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: US 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage Q-beta
 US-10-465-811-2

Query Match 100.0%; Score 1749; DB 15; Length 329;
 Best Local Similarity 100.0%; Pred. No. 3.8e-161;
 Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTGNGKDGKQTLVNPGRVPTNGVSLQAGVPALEKRVTVSVQPSRRR 60
 DB 1 MAKETVTGNGKDGKQTLVNPGRVPTNGVSLQAGVPALEKRVTVSVQPSRRR 60
 QY 61 KKKYQVKIQNPTACTANGSCDPSVTROAYADVTSFTQYSTDERAFVRTLAALLASP 120
 DB 61 KKKYQVKIQNPTACTANGSCDPSVTROAYADVTSFTQYSTDERAFVRTLAALLASP 120
 QY 121 LIIDAIIDQNPAYWTLILAGGSGSKPDVIPPDPIDPPGIGKTCPPAIIWSLEEVYP 180
 DB 121 LIIDAIIDQNPAYWTLILAGGSGSKPDVIPPDPIDPPGIGKTCPPAIIWSLEEVYP 180
 QY 181 PTKNRPPIYNAVELQPREFDVALKDLGNTKMRDWSLSYTPRGCRNGYIDDATY 240
 DB 181 PTKNRPPIYNAVELQPREFDVALKDLGNTKMRDWSLSYTPRGCRNGYIDDATY 240
 QY 241 LATDQMRDQKDIIEGKKPGAFGNIERIYIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
 DB 241 LATDQMRDQKDIIEGKKPGAFGNIERIYIYKSIINAYCSLSDIAAYHADGVIYGFWRDP 300
 QY 301 SSGGAIIPDFTKEDTKCPICQAVIYVPPRA 329
 DB 301 SSGGAIIPDFTKEDTKCPICQAVIYVPPRA 329

RESULT 6

US-10-289-456-11
 ; Sequence 11, Application US/10289456
 ; Publication No. US20040033211A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Spohn, Gunther
 ; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
 ; FILE REFERENCE: 1700.0330001
 ; CURRENT APPLICATION NUMBER: US/10/289,456
 ; CURRENT FILING DATE: 2002-11-07
 ; PRIOR APPLICATION NUMBER: PCT/IB02/00166
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 10/050,902
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/396,635
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: US 60/331,045
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 11
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage Q-beta
 US-10-289-456-11

Query Match 100.0%; Score 1749; DB 15; Length 329;
 Best Local Similarity 100.0%; Pred. No. 3.8e-161;
 Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTGNGKDGKQTLVNPGRVPTNGVSLQAGVPALEKRVTVSVQPSRRR 60
 DB 1 MAKETVTGNGKDGKQTLVNPGRVPTNGVSLQAGVPALEKRVTVSVQPSRRR 60

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Db      1 MAKLETVTLGNIGKDGKQTLVLPNPGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNR 60
Qy      61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVTSFTQYSTDERAFVRETELALLASP 120
Db      61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVTSFTQYSTDERAFVRETELALLASP 120
Qy      121 LIIDAIDQNPAYWTLIIAGGSGSKDPVIPPDPIDPPGTGKTCFPAIWSLEEVYEP 180
Db      121 LIIDAIDQNPAYWTLIIAGGSGSKDPVIPPDPIDPPGTGKTCFPAIWSLEEVYEP 180
Qy      181 PTKNRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTPRGCRNGYIDLDTATY 240
Db      181 PTKNRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTPRGCRNGYIDLDTATY 240
Qy      241 LATDQAMRDQKDIIEGKKRGAFGNIERFIYLSINAYCSLDIAAYHADGVIYGFWRDP 300
Db      241 LATDQAMRDQKDIIEGKKRGAFGNIERFIYLSINAYCSLDIAAYHADGVIYGFWRDP 300
Qy      301 SSGAIPDFPTKDKTCPIQAVIVPRA 329
Db      301 SSGAIPDFPTKDKTCPIQAVIVPRA 329

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RESULT 7

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US-10-622-064-4
; Sequence 4, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Qbeta
US-10-622-064-4

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Query Match      100.0%; Score 1749; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAKLETVTLGNIGKDGKQTLVLPNPGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNR 60
Db      1 MAKLETVTLGNIGKDGKQTLVLPNPGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNR 60
Qy      61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVTSFTQYSTDERAFVRETELALLASP 120
Db      61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVTSFTQYSTDERAFVRETELALLASP 120
Qy      121 LIIDAIDQNPAYWTLIIAGGSGSKDPVIPPDPIDPPGTGKTCFPAIWSLEEVYEP 180
Db      121 LIIDAIDQNPAYWTLIIAGGSGSKDPVIPPDPIDPPGTGKTCFPAIWSLEEVYEP 180
Qy      181 PTKNRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTPRGCRNGYIDLDTATY 240
Db      181 PTKNRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTPRGCRNGYIDLDTATY 240
Qy      241 LATDQAMRDQKDIIEGKKRGAFGNIERFIYLSINAYCSLDIAAYHADGVIYGFWRDP 300
Db      241 LATDQAMRDQKDIIEGKKRGAFGNIERFIYLSINAYCSLDIAAYHADGVIYGFWRDP 300
Qy      301 SSGAIPDFPTKDKTCPIQAVIVPRA 329
Db      301 SSGAIPDFPTKDKTCPIQAVIVPRA 329

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RESULT 8

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US-10-622-124-5
; Sequence 5, Application US/10622124
; Publication No. US20040076645A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulturja, Alma
; TITLE OF INVENTION: Ghrelin-Carrier Conjugates
; FILE REFERENCE: 1700.0340001
; CURRENT APPLICATION NUMBER: US/10/622,124
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,638
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-622-124-5

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Query Match      100.0%; Score 1749; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAKLETVTLGNIGKDGKQTLVLPNPGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNR 60
Db      1 MAKLETVTLGNIGKDGKQTLVLPNPGVNPPTNGVASLSQAGAVPALERKVTVSQPSRNR 60
Qy      61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVTSFTQYSTDERAFVRETELALLASP 120
Db      61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVTSFTQYSTDERAFVRETELALLASP 120
Qy      121 LIIDAIDQNPAYWTLIIAGGSGSKDPVIPPDPIDPPGTGKTCFPAIWSLEEVYEP 180
Db      121 LIIDAIDQNPAYWTLIIAGGSGSKDPVIPPDPIDPPGTGKTCFPAIWSLEEVYEP 180
Qy      181 PTKNRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTPRGCRNGYIDLDTATY 240
Db      181 PTKNRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSYTPRGCRNGYIDLDTATY 240
Qy      241 LATDQAMRDQKDIIEGKKRGAFGNIERFIYLSINAYCSLDIAAYHADGVIYGFWRDP 300
Db      241 LATDQAMRDQKDIIEGKKRGAFGNIERFIYLSINAYCSLDIAAYHADGVIYGFWRDP 300
Qy      301 SSGAIPDFPTKDKTCPIQAVIVPRA 329
Db      301 SSGAIPDFPTKDKTCPIQAVIVPRA 329

```

RESULT 9

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US-10-622-087-5
; Sequence 5, Application US/10622087
; Publication No. US20040141984A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tisoc, Alain
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Mathias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
; FILE REFERENCE: 1700.0350002
; CURRENT APPLICATION NUMBER: US/10/622,087
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,639
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/470,432
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 329

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TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-622-087-5

Query Match 100.0%; Score 1749; DB 16; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.8e-161;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKETVTLGNIGKQKQTLVLPNGVNTNGVASISQAGVPALEKRTVSVSOPSRNR 60
DB 1 MAKETVTLGNIGKQKQTLVLPNGVNTNGVASISQAGVPALEKRTVSVSOPSRNR 60
QY 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDBERAFTRTIELAALLASP 120
DB 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDBERAFTRTIELAALLASP 120
QY 121 LIIIDAIDQNPAYWTLIIAGGSGSKPDVPIPDPPGKGTCTCPAIVMSLEEVYP 180
DB 121 LIIIDAIDQNPAYWTLIIAGGSGSKPDVPIPDPPGKGTCTCPAIVMSLEEVYP 180
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTTRGCGNGYIDLATY 240
DB 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTTRGCGNGYIDLATY 240
QY 241 LATDQAMRDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 300
DB 241 LATDQAMRDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 300
QY 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329
DB 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329

RESULT 10
US-10-243-739-11

; Sequence 11, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornli, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243, 739
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318, 967
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-11

Query Match 99.1%; Score 1733.5; DB 14; Length 328;
Best Local Similarity 99.7%; Pred. No. 1.2e-159;
Matches 328; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAKETVTLGNIGKQKQTLVLPNGVNTNGVASISQAGVPALEKRTVSVSOPSRNR 60
DB 1 MAKETVTLGNIGKQKQTLVLPNGVNTNGVASISQAGVPALEKRTVSVSOPSRNR 60
QY 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDBERAFTRTIELAALLASP 120
DB 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDBERAFTRTIELAALLASP 120
QY 121 LIIIDAIDQNPAYWTLIIAGGSGSKPDVPIPDPPGKGTCTCPAIVMSLEEVYP 180
DB 121 LIIIDAIDQNPAYW-TLIIAGGSGSKPDVPIPDPPGKGTCTCPAIVMSLEEVYP 179
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTTRGCGNGYIDLATY 240

DB 180 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTTRGCGNGYIDLATY 239
QY 241 LATDQAMRDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 300
DB 240 LATDQAMRDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 299
QY 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329
DB 300 SSGGAIIPDFTKFDKTCPIQAVIVPRA 328

RESULT 11
US-10-244-065-11

; Sequence 11, Application US/10244065
; Publication No. US20030099688A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornli, Tazio
; APPLICANT: Maurel, Patrick
; APPLICANT: Tisot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumpens, Paul
; APPLICANT: Cieleus, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244, 065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374, 145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318, 994
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-11

Query Match 99.1%; Score 1733.5; DB 14; Length 328;
Best Local Similarity 99.7%; Pred. No. 1.2e-159;
Matches 328; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAKETVTLGNIGKQKQTLVLPNGVNTNGVASISQAGVPALEKRTVSVSOPSRNR 60
DB 1 MAKETVTLGNIGKQKQTLVLPNGVNTNGVASISQAGVPALEKRTVSVSOPSRNR 60
QY 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDBERAFTRTIELAALLASP 120
DB 61 KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTSFTQYSTDBERAFTRTIELAALLASP 120
QY 121 LIIIDAIDQNPAYWTLIIAGGSGSKPDVPIPDPPGKGTCTCPAIVMSLEEVYP 180
DB 121 LIIIDAIDQNPAYW-TLIIAGGSGSKPDVPIPDPPGKGTCTCPAIVMSLEEVYP 179
QY 181 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTTRGCGNGYIDLATY 240
DB 180 PTKNRPWPIYNAVELQPREFDVALKDLGNTKMRDMSRLSTTTRGCGNGYIDLATY 239
QY 241 LATDQAMRDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 300
DB 240 LATDQAMRDQKYDIREGKKPGAFGNIERFIYKSIINAYCSLSIDIAAYHADGVIYGFWRDP 299
QY 301 SSGGAIIPDFTKFDKTCPIQAVIVPRA 329
DB 300 SSGGAIIPDFTKFDKTCPIQAVIVPRA 328

RESULT 12
US-10-243-739-16
Sequence 16, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazilo
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243, 739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318, 967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 329
TYPE: PRT
ORGANISM: Bacteriophage SP
US-10-243-739-16

Query Match 55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred. No. 3, 4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY 2 AKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRRNK 61
DB 1 AKLNQVTLSTKIGKNDQTLTPRGVPTNGVASLSQAGAVPALERKVTVSQPSRRNK 60
QY 62 NYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTEIAALLASPL 121
DB 61 NFKVQIKIQNPACTRD-ACDPSVTRSAFADVTLSTFTSTDEBERALIRTEIAALLADPL 119
QY 122 LIDAIDQNPAYW-TLLIAGGSGSKPD---EVLPDPIDPPPTGKTCTCPAIVSLSE 176
DB 120 IYDAIDNINPAYWALLVASSGGGNDPDPVPVVD--VKPPDGTGRYKCFACRYLGS 177
QY 177 VPEPTKRPMPVYNVAVELQPREFDVALKDLGNTKMDPSRLS---YTFPGCRGNGY 233
DB 178 IYEVGKESGP-DIYRGDEVSTFEDYALDEPLGNTNMNDQRLSDYIANRRRCRGNGY 236
QY 234 IDLDATYLATDQMRDQKDIYREGKPKGAGNIEFTYLSI--NAVCSLSDIAAYHADG 291
DB 237 IDLDATAMQSDDFVLSGRYGVKVKFPGAFGSIK---YLLNIGDAMLDLSEVTAYRSYG 293
QY 292 VIVGFWRPSSGGAIPDPFTKFDKTCPIQAVIYVP 327
DB 294 NVIGFWTD-SKSPQLPFDFTQFNSANCPVQTVIILP 328

RESULT 13
US-10-244-065-16
Sequence 16, Application US/10244065
Publication No. US20030099668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazilo
APPLICANT: Maurer, Patrick
APPLICANT: Tassot, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cieles, Indulis
APPLICANT: Renhota, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244, 065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374, 145

PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318, 994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 329
TYPE: PRT
ORGANISM: Bacteriophage SP
US-10-244-065-16

Query Match 55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred. No. 3, 4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY 2 AKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRRNK 61
DB 1 AKLNQVTLSTKIGKNDQTLTPRGVPTNGVASLSQAGAVPALERKVTVSQPSRRNK 60
QY 62 NYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTEIAALLASPL 121
DB 61 NFKVQIKIQNPACTRD-ACDPSVTRSAFADVTLSTFTSTDEBERALIRTEIAALLADPL 119
QY 122 LIDAIDQNPAYW-TLLIAGGSGSKPD---EVLPDPIDPPPTGKTCTCPAIVSLSE 176
DB 120 IYDAIDNINPAYWALLVASSGGGNDPDPVPVVD--VKPPDGTGRYKCFACRYLGS 177
QY 177 VPEPTKRPMPVYNVAVELQPREFDVALKDLGNTKMDPSRLS---YTFPGCRGNGY 233
DB 178 IYEVGKESGP-DIYRGDEVSTFEDYALDEPLGNTNMNDQRLSDYIANRRRCRGNGY 236
QY 234 IDLDATYLATDQMRDQKDIYREGKPKGAGNIEFTYLSI--NAVCSLSDIAAYHADG 291
DB 237 IDLDATAMQSDDFVLSGRYGVKVKFPGAFGSIK---YLLNIGDAMLDLSEVTAYRSYG 293
QY 292 VIVGFWRPSSGGAIPDPFTKFDKTCPIQAVIYVP 327
DB 294 NVIGFWTD-SKSPQLPFDFTQFNSANCPVQTVIILP 328

RESULT 14
US-10-289-454-16
Sequence 16, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderogger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289, 454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396, 636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050, 902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331, 045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 329
TYPE: PRT
ORGANISM: Bacteriophage SP CP
US-10-289-454-16

Query Match 55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred. No. 3, 4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY 2 AKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSRRNK 61


```

Db      1 AKLNGVTLSKIGKNDQTLTLTPRGVNPNGVASLSSEAGAVPALERKRVTSVAQPSRNK 60
Qy      62 NYKVQVIONPACTANGSCDPSVTRQAYADYTFSTQSTDEBRFAVTELAALLASPL 121
Db      61 NFKVQIKONPACTARD-ACDPSVTRSAFADYTLSTSTDEBRLLITELALALADPL 119
Qy      122 LIDAIQOLNPAYW-TLLIAGGSGSKPD---FVLPDPIDPPPGTKYTCFPAIWSLEB 176
Db      120 IYDAIDNINPAYWALLVASSGGGNDPSPDPVVPD--VKPPDGTGRKCPACRYLGS 177
Qy      177 VYEPPTKRPMPPIYNAVELQPREFDVALKOLLGNTKRWDSRLS---YTTFRGCRNGY 233
Db      178 IYEVGKEGSP-DIYERGDEVSVTFDYALDFLGNTNMRWMDQRLSDYDIANRRRCRNGY 236
Qy      234 IDLDATYLATQAMRDQKYDIREGKKPGAFGNIERFIYLSI--NAYCSLSIDIAAYHADG 291
Db      237 IDLDATAMQSDPFVLSGRYGVAKVFPAGAFSGIK--YLLNTIQGDMWLDLSEVTAYRSYG 293
Qy      292 VIVGFWRDPSSGGAIPFDFTKFKDKTKCPIQAVIYVP 327
Db      294 WVIQFWTD-SKSPQLPTDFTQFNNSANCPVQTVIIIP 328

```

```

RESULT 15
US-10-346-190-16
; Sequence 16, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurel, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 329
; TYPE: prt
; ORGANISM: RNA-phase SP A1 protein
US-10-346-190-16

```

```

Query Match      55.9%; Score 978; DB 14; Length 329;
Best Local Similarity 58.3%; Pred. No. 3,4e-86;
Matches 196; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

```

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Qy      2 AKLETVTLGNIKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALERKRVTSVQPSRNK 61
Db      1 AKLNGVTLSKIGKNDQTLTLTPRGVNPNGVASLSSEAGAVPALERKRVTSVAQPSRNK 60
Qy      62 NYKVQVIONPACTANGSCDPSVTRQAYADYTFSTQSTDEBRFAVTELAALLASPL 121
Db      61 NFKVQIKONPACTARD-ACDPSVTRSAFADYTLSTSTDEBRLLITELALALADPL 119
Qy      122 LIDAIQOLNPAYW-TLLIAGGSGSKPD---FVLPDPIDPPPGTKYTCFPAIWSLEB 176
Db      120 IYDAIDNINPAYWALLVASSGGGNDPSPDPVVPD--VKPPDGTGRKCPACRYLGS 177
Qy      177 VYEPPTKRPMPPIYNAVELQPREFDVALKOLLGNTKRWDSRLS---YTTFRGCRNGY 233

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Db      178 IYEVGKEGSP-DIYERGDEVSVTFDYALDFLGNTNMRWMDQRLSDYDIANRRRCRNGY 236
Qy      234 IDLDATYLATQAMRDQKYDIREGKKPGAFGNIERFIYLSI--NAYCSLSIDIAAYHADG 291
Db      237 IDLDATAMQSDPFVLSGRYGVAKVFPAGAFSGIK--YLLNTIQGDMWLDLSEVTAYRSYG 293
Qy      292 VIVGFWRDPSSGGAIPFDFTKFKDKTKCPIQAVIYVP 327
Db      294 WVIQFWTD-SKSPQLPTDFTQFNNSANCPVQTVIIIP 328

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Search completed: January 4, 2005, 09:41:21
Job time : 82.5897 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 19.6637 Seconds

(without alignment)
1609.836 Million cell updates/sec

Title: US-10-622-064-4

Perfect score: 1749
Sequence: 1 MAKETVTLGNIGKDGKQTL.....FTKPKTKCP1QAVIVPRA 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	983	56.2	331	2	readthrough protei
2	663	37.9	132	1	coat protein - pha
3	117	6.7	131	1	coat protein - pha
4	113.5	6.5	409	2	conserved hypotet
5	106	6.1	973	2	probable secreted
6	95.5	5.4	1326	2	probable ATP-depen
7	95	5.4	915	2	cellulase (EC 3.2.
8	94.5	5.4	530	2	seeligerolysin -
9	94	5.4	501	2	growth/differentia
10	93.5	5.3	540	2	hypothetical prote
11	93	5.3	439	2	glutamine syntheta
12	93	5.3	974	1	optic lobe develop
13	92.5	5.3	983	2	polymorphic membra
14	92	5.3	385	2	hypothetical prote
15	91.5	5.2	1461	2	hypothetical prote
16	91.5	5.2	1461	2	hypothetical prote
17	91	5.2	609	2	hypothetical prote
18	90.5	5.2	280	2	transcription fact
19	90.5	5.2	836	2	hypothetical prote
20	90.5	5.2	836	2	hypothetical prote
21	90.5	5.2	1302	2	hypothetical prote
22	90.5	5.2	1785	2	hypothetical prote
23	90	5.1	495	2	major merizote su
24	90	5.1	1569	2	bone morphogenetic
25	90	5.1	1612	2	hypothetical prote
26	89.5	5.1	341	2	ductil protein - mo
27	89.5	5.1	529	2	probable tellurium
28	89.5	5.1	529	2	listeriolysin prec
29	89.5	5.1	529	2	listeriolysin O pr
					listeriolysin O pr

30	89	5.1	949	2	T08658	hypothetical prote
31	89	5.1	1039	2	S02711	cellulase (EC 3.2.
32	88.5	5.1	830	2	S57537	MKRI protein - yea
33	88.5	5.1	1307	2	T35944	probable beta-gala
34	88	5.0	928	2	C81265	probable lipoprote
35	88	5.0	978	2	D81411	probable lipoprote
36	87	5.0	346	2	B60340	transposase - Myco
37	87	5.0	346	2	H70567	transposase - Myco
38	86.5	4.9	476	2	B44997	merozoit surface
39	86.5	4.9	593	2	F64523	hypothetical prote
40	86	4.9	130	1	A46324	coat protein - pha
41	86	4.9	408	2	S54813	probable chain len
42	86	4.9	793	2	T41703	dipeptidyl aminope
43	86	4.9	850	2	S56015	gastric mucin MUC5
44	86	4.9	933	2	S41539	fibrinogen-binding
45	85.5	4.9	312	2	A56911	TRAD protein - hu

ALIGNMENTS

RESULT 1

readthrough protein - phage SP

C/Species: phage SP
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S01964
R/Inokuchi, Y.; Jacobson, A.B.; Hirose, T.; Inayama, S.; Hiraehima, A.

Nucleic Acids Res. 16, 6205-6221, 1988

A/Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP.

A/Reference number: S01963; MUID:88289362; PMID:3399390

A/Accession: S01964

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-331 <INO>

A/Cross-references: UNIPROT:P09677, EMBL:X07489

A/Note: the authors translated the readthrough stopcodon TGA for residue 133 as Trp

C/Superfamily: phage GA coat protein

Query Match	Score	983	DB 2	Length	331	Indels	18	Gaps	9
Best Local Similarity	56.2%								
Matches	197								
Conservative	45								
Mismatches	77								
QY	1	MAKETVTLGNIGKDGKQTLVLPNGVNPNGVNLASQAGVPALEKRVTVSVSOPSRNR	60						
DB	1	MAKNQVTLSTKIGKNGDDTLITPRGVNPTNGVNLASQAGVPALEKRVTVSVSOPSRNR	60						
QY	61	KNYKVQVKIQNFTACTANGSCDPSVTRQAVADVTFTQYSTDBERAFVRIELALLASP	120						
DB	61	KNFKVQIKIQNFTACTARD-ACDPSVTRSAFADVTLSFTSYSTDBERALLRIELALLADP	119						
QY	121	LILDAIDQNPAYW-TLIIAGGSGSKPD---PYIPDPIDPPGTCGYTCPPAIVSL	175						
DB	120	LIVDAIDNPAYWALLVASSGGSDNPDPVPVPPD-VPPPGTGKVPKPCYRIRG	177						
QY	176	EYEPPTKRPPIYNAVELQPREPVALKDLIGTKRMDMSRLS---YTFPGCRGNG	232						
DB	178	STYEVKSGSP-DIERGDVSVTFDVALLEDLIGTKRMDMSRLS---YTFPGCRGNG	236						
QY	233	YIDDATYIADQANDQKIDIRBKKPGAFNIRFFYLSI---NAYCSLDIAAHHAD	290						
DB	237	YIDLDATAMQSDPFLSGRYGVKVPFGAFSGISK---YLIINIQDAMWLSEVAYRSY	293						
QY	291	GIVVGFWRDPSGGAIPDFTEKEDTKCP1QAVIVVP	327						
DB	294	GVVGFWRD-SKSPFLPTDFQNSANCPVQTVIIP	329						

RESULT 2
VCBPOB
coat protein - phage Q-beta
C/Species: phage Q-beta
C/Date: 29-Jul-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004

C/Accession: A92240; A92221; A92088; A04224
 R/Bacarris, C.; Saeary, P.A.; Billeter, M.A.
 J. Biol. Chem. 253, 8390-8399, 1978
 A/Title: Determination of the first half of the coat protein cistron of bacteriophage Q
 A/Reference number: A92240; MID:79048469; PMID:361741
 A/Accession: A92240
 A/Molecule type: mRNA
 A/Residues: 1-80 <SEC>
 A/Cross-references: UNIPROT:P03615
 R/Stoll, E.; Wilson, K.J.; Reiser, J.; Weissmann, C.
 J. Biol. Chem. 252, 990-993, 1977
 A/Title: Reversed amino acid sequence of Qbeta coat protein between positions 1 and 60.
 A/Reference number: A92221; MID:77118576; PMID:838709
 A/Accession: A92221
 A/Molecule type: protein
 A/Residues: 1-60 <STO>
 R/Maita, T.; Konigsberg, W.
 J. Biol. Chem. 246, 5003-5024, 1971
 A/Title: The amino acid sequence of the Qbeta coat protein.
 A/Reference number: A92088; MID:71288580; PMID:5570434
 A/Accession: A92088
 A/Molecule type: protein
 A/Residues: 1-21; D, 23-55, 57-132 <MAI>
 C/Superfamily: phage GA coat protein

Query Match 37.9%; Score 663; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKLETVTLNIGKDGKQTLVLPNGVNPITNGVSLSQAGVPALEKRVTVSVSQPSRNK 61
 DB 1 AKLETVTLNIGKDGKQTLVLPNGVNPITNGVSLSQAGVPALEKRVTVSVSQPSRNK 60
 QY 62 NYVQVKIONPTACTANGSCDPSVTROAVDVTFSTQYSTDERAFVTELAALLASPL 121
 DB 61 NYVQVKIQNPVACTANGSCDPSVTROAVDVTFSTQYSTDERAFVTELAALLASPL 120
 QY 122 LIDAIQDQNPAY 133
 DB 121 LIDAIQDQNPAY 132

RESULT 3
 VCBPPI
 coat protein - phage PRRI
 C/Species: phage PRRI
 C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
 R/Accession: A04225
 R/Dhaese, P.; Vandekerckhove, J.S.; Van Montagu, M.C.
 Eur. J. Biochem. 94, 375-386, 1979
 A/Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage Q
 A/Reference number: A04225; MID:79148387; PMID:107028
 A/Accession: A04225
 A/Molecule type: protein
 A/Residues: 1-131 <DNA>
 A/Cross-references: UNIPROT:P03616
 C/Superfamily: phage GA coat protein

Query Match 6.7%; Score 117; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.011;

Matches 42; Conservative 15; Mismatches 57; Indels 16; Gaps 5;

QY 18 QTLVLPNGVNPITACTANGSCDPSVTROAVDVTFSTQYSTDERAFVTELAALLASPL 67
 DB 4 QNLVLDKREKTPMDHFTVPDIDNNGEVESTGVPIGESRFTISLRKISNGR--YKSTL 61
 QY 68 KIONPT-ACTANGSCDPSVTROAVDVTFSTQYSTDERAFVTELAALLASPL 123
 DB 62 KLVVPVQSGTVNGIVTPVVPVTSYTVDPDARSTKERNFVGMIALADALMLVH 121
 QY 124 DAIDQDQNPAY 133
 DB 122 DTIVNLQGVY 131

RESULT 4
 D90268
 conserved hypothetical protein [imported] - Sulfolobus solfataricus

C/Species: Sulfolobus solfataricus
 C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C/Accession: D90268
 R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y
 Jung, I.; Jeffries, A.C.; Konner, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
 arret, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to Genbank, April 2001
 A/Description: Sulfolobus solfataricus complete genome.
 A/Reference number: A99139
 A/Accession: D90268
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-409 <KUR>
 A/Cross-references: UNIPROT:Q97Y27; GB:AE00641; NID:G13814341; PIDN:AAK1403.1; GSPDB:G

A/Genetics: SSO1152
 A/Genes: SSO1152

Query Match 6.5%; Score 113.5; DB 2; Length 409;
 Best Local Similarity 23.0%; Pred. No. 0.096;

Matches 62; Conservative 36; Mismatches 99; Indels 73; Gaps 13;

QY 89 AVADVTFSPTQYSTDERAFVTELAAL-----LASPL-----LIDAIQDQNP 131
 DB 160 AFSSTSFSSQYKDSIKKA---NELASITGKYEITGKXVDLSPLVMGNLMESVARNAS 216
 QY 132 AY-----WTLIAGGSGSKDPVIPPDP-----PQT-----GKYTCF 169
 DB 217 GYAIMSGMSMLKPGKAGSDKFTLLDTPKEDRPNMGPDDECTFYNNKAIINGVFTPL 276
 QY 170 AIMSLEBYE-PPTKNRPPIYNAVELQREEDVALKDLG-----NTKMDWDSRLSX 222
 DB 277 LNNEISNVFKLPSTGAGNITYPTANMLEVEDTSPESILSGNVVFYINVM-----Y 328
 QY 223 TFRGCGNGYIDLATYLATDQAMRDQYDIREGKPGAPGNIRFIYKISINAYCSLS 282
 DB 329 TRFQ-----NVAEGPSTVA-----RDATVYVRNGNPGVIGRVLADNLKRI-----LK 373
 QY 283 DIAAHADGVIVGFMRDPSGGAIPDPFK 312
 DB 374 NIVELSRERYSVRWMDAPWQ-GVYPYALVK 402

RESULT 5

T35238
 probable secreted cellulase - Streptomyces coelicolor

C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C/Accession: T35238
 R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, September 1998
 A/Reference number: Z21572
 A/Accession: T35238
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-973 <SEB>
 A/Cross-references: UNIPROT:O86728; EMBL:AL01515; PIDN:CAA20643.1; GSPDB:GN00070; SGOEDB
 A/Experimental source: strain A3(2)
 C/Genetics: A/Genes: SGOEDB:SC05C7.31c

Query Match 6.1%; Score 106; DB 2; Length 973;
 Best Local Similarity 23.4%; Pred. No. 1.3;

Matches 47; Conservative 24; Mismatches 86; Indels 44; Gaps 10;

QY 138 IAGGSGSKDPVIPPDPDPGNGKYCPAISMSEVPEPTKN-----RPMPIYNA 192
 DB 717 IAGGATNSAGR-YATPAGTPTFGMY-----YDEKTVYHDPDSNGMFGQANSMERV 769

QY 193 VELQREPFVVLKDLGNTKRDWMSRLSYTTPRCGRNGYIDLDTATYATDQAMDDQKY 252
 Db 770 AEYQOOSGAGAKAVL--DKWVDM--ALSEET-----VNPDETFPIPSLTQWSSGP 816
 QY 253 DUREGKKPGAFG--NIEFTYLSKINAYCSLSDIAYHAD-----GVIVGFWR 298
 Db 817 DTMNASSPANGDDHVEVDYTNVDGVAAAYAKTLTYADRSQDTBAASTARALLDGMWE 876
 QY 299 D--PSSGAIP--FDPTKFD 314
 Db 877 NNQDALGIAPVETRADYNNRFD 897

RESULT 6

H83232
 Probable ATP-dependent helicase PA3297 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #ext_change 09-Jul-2004
 C:Accession: H83232
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: AB2950; MUID:20437357; PMID:10984043
 A:Accession: H83232
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1326 <STO>
 A:Cross-references: UNIPROT:Q9HYI6; GB:AE004752; GB:AE004091; NID:G9949424; PIDN:AA60668
 A:Experimental source: strain PA01
 A:Gene: PA3297

Query Match 5.4%; Score 95.5; DB 2; Length 1326;
 Best Local Similarity 24.9%; Pred. No. 15;

Matches 92; Conservative 48; Mismatches 124; Indels 105; Gaps 25;

QY 17 KQTLVLPNG-----VNPNGVAVSLQAGAVPALEKEKVTAVSQPSHNRKRYKVQ-VKION 71
 Db 338 EQQKIFQPRPKRKYVSTN-VAETSL--TVPGIRYVDSGTARISRYRAKQRLPIEA 394
 QY 72 PFACTAN-----GSCDPSVTRQAVDVTFSTQYSTDEBARFRTLAALLASPL--- 122
 Db 395 VQASANQKRGKRCGRVEPGICVRLYSEBDFNAPARTDE--ILRTNLAAILQMLRL 452
 QY 123 --IDAIDQANPA-----YMTLL--IAGGSGSKDDPV--IPDPPIPPRG----- 161
 Db 453 GDIKAPFTEPPDGKAIKDGFTLLQELSAVNRGQLTPGROARLPIDPRIGRMLEEA 512
 QY 162 -TGKATCPFAIWSLEBEVPEPTKRPMPYNAVELQ--PREFVALKDL--GNTKWRMD 217
 Db 513 QQG-----SLEBVL-----TYASALSVDPREPRPERQADDAQMAQMKDPD 554
 QY 218 SRLS--YTFRG-----CRGN--GYIDL--DA--TYLATDQAM-- 247
 Db 555 SDFALINIMRGREBQROALGSNALRSWCKNFPLNTLRLEWMDARQLTLICRELKLP 614
 QY 248 -RDQKIDIEGK-KPAFNGIERFT---YLSINAYCS--LSDIAYHADGVIVG----- 295
 Db 615 GPPAKAKAPKPKKAGASADNREVPIDYAAVHAKILGSLSQLQOKAEBGDYLGAROR 674
 QY 296 -FWRDPSSG 303
 Db 675 RFWIHPSG 683

RESULT 7

AA3802
 cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellulohydrolase (EC 3.2.1.91) - Caldocellum
 N:Alternate names: endo-1,4-beta-glucanase
 C:Species: Caldocellum saccharolyticum
 C>Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #ext_change 15-Mar-2004

C:Accession: AA3802
 R:Saul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L.
 Appl. Environ. Microbiol. 56, 3117-3124, 1990
 A:Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile "C
 A:Reference number: AA3802; MUID:91136262; PMID:2126700
 A:Accession: AA3802
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
 A:Molecule type: DNA
 A:Residues: 1-915 <SAU>
 A:Cross-references: EMBL:X13602
 C:Function:
 A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cel
 A:Pathway: cellulose degradation
 A:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:20-320/Domains: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

Query Match 5.4%; Score 95; DB 2; Length 915;
 Best Local Similarity 22.1%; Pred. No. 10;

Matches 54; Conservative 38; Mismatches 108; Indels 44; Gaps 12;

QY 90 YADVTFSTQYSTDEBARFRTLAALLASPLIDAIDLPNAVYTLIAGGSGSKPDP 149
 Db 271 YKNVKSVMFQGLKDDYSMLRS-FYKNDWPLLFEDYSAKAYAVMAVIEASGVTTSSPTP 329
 QY 150 -----VLPDPIDPPPGTGKTYTCFPAIWSLEBEVPEPTKRPMPYNAVELQREFV 202
 Db 330 TPTPTVTVTPPTPTPTPG-GQIK--VYANKETNSTNTNTRPW--LRVNSGSSSIDL 383
 QY 203 ALKDLGNTKRDWMSRLSYTTPRCGRNGYIDLDTATYATDQAMDDQKYDIREGKPGA 262
 Db 384 SRVTI--RYWTVDERQASVSDWAQIGASVTFPFYKLSSVSGADYILEIGKSGA 440
 QY 263 -----FGNIE-RF-----IYKLSINAYCSLDIAYHADGVIVGFW-R 298
 Db 441 GOLQPKDQGEIQIRNKSDMSNNGNDMSWMLQSTISGEMEKVAY-IDGLV--WQ 497
 QY 299 DPSS 302
 Db 498 EPST 501

RESULT 8

S22340
 seeligeriolysin - Listeria seeligeri
 C:Species: Listeria seeligeri
 C>Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #ext_change 09-Jul-2004
 C:Accession: S22340
 R:Haas, A.; Dumbeky, M.; Kreft, U.
 Biochim. Biophys. Acta 1130, 81-84, 1992
 A:Title: Listeriolysin genes: complete sequence of *llo* from *Listeria ivanovii* and of *lso*
 A:Reference number: S22340; MUID:92182018; PMID:1543752
 A:Accession: S22340
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-530 <HAA>
 A:Cross-references: UNIPROT:P31830; EMBL:X60462; NID:G44144; PIDN:CAA42996.1; PID:G44145
 A:Note: the authors translated the codon GCC for residue 287 as Pro
 C:superfamily: dipeptide transport protein

Query Match 5.4%; Score 94.5; DB 2; Length 530;
 Best Local Similarity 25.8%; Pred. No. 5.4;
 Matches 34; Conservative 23; Mismatches 40; Indels 35; Gaps 7;

QY 14 KQKQKTLV--NPRGVNPT-----NGVASISQGA-----VPALEKRY 49
 Db 94 KDGSEYIVKPKKKGINNNADISVINATISLTPPALVYKANRELVENPNVLPVKRDSL 153
 QY 50 TVSVQPSNRKRYKQVQKIONPTACTANGSCDPSVTR-----QAYADVTFSTQYSTD 103
 Db 154 TISVDLPQMTKKDKNKIFVR--NPTKSNVNAVNTLVERKNDKSKAYPIVINKI-DYS-- 208
 QY 104 EEPAYRTLEAA 115

DB 209 DENAYESOLIA 220

RESULT 9

JC2347 growth/differentiation factor 5 - human

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: JC2347

R/Author: G. J. Neidhardt, H. J. Jacobowsky, B. J. Pohl, J.

Biochem. Biophys. Res. Commun. 204, 646-652, 1994

A/Title: Cloning and expression of recombinant human growth/differentiation factor 5.

A/Reference number: JC2347; PMID:95071375; PMID:7980526

A/Accession: JC2347

A/Molecule type: DNA

A/Residues: 1-501 <HOE>

A/Cross-references: UNIPROT:P43026; GB:X80915; NID:g671524; PIDN:CAA56874.1; PID:g671525

C/Genetics:

A/Genes: GDB:BM9

A/Cross-references: GDB:433948

A/Introns: 211/1

C/Superfamily: inhibitor

C/Keywords: glycoprotein

F/89/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 5.4%; Score 94; DB 2; Length 501;

Best Local Similarity 21.7%; Pred. No. 5.5; Mismatches 115; Indels 128; Gaps 18;

Matches 77; Conservative 35; Mismatches 115; Indels 128; Gaps 18;

22 LNRGVNPTNGVSLQAGAVP-----ALEKRVTVSVQSPR----- 58

122 VPKGQLP--GKAPKAGSVSPSFLKKAREGPPEPRPPPTTPEHYMLSLYR 179

59 -----NRKNVQVQKIQNPACTANGSCD-----PSYTRQAAV-DYTFSTQYSDER 106

180 LSDADKKGNSVYLEGLANTTSTFDKQDDRGFPVKKQYVFDI-----SALKEK 232

107 AFVTEIAALLAPLIDALDQNPVWTLIAGG-----SGSKPPVPIPDPP 155

233 GLGALRLIRKKP-----SDTAKPA-----APGGRAAQLKISCSGSGPASLIDVR 282

156 IDPPGTGKTCPPAIWSLEVEYEPPTKN-----RPPIYNAVELQPREVDALKD- 206

283 VPLDSDSGWEV--FDIMKLFRRN-----KNSAQLCLELAWEGRADVLRGLGFDRAARQV 336

207 -----LIGNTKWRWDSRLSYTTRGCGNGYIDLDAT--YLAITDQMRDQKTDIRE 256

337 HEKALPLVGRTRKRD-----LFNEIKANSQD-----DKTYEYLSQKRRKRAPIATRO 388

257 GKKGAFGNIERPIYLSKINAYCSLS-----DIAAYHADV 292

389 GKRRS-----KNLKARCSRKALHYNFKMGMDWITIALEAEAFHCEGL 432

RESULT 10

T00646 hypothetical protein F316.9 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C/Accession: T00646

R/Author: N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo, R.; Federspiel, N.A.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.

submitted to the EMBL Data Library, February 1998

A/Reference number: Z14197

A/Accession: T00646

A/Status: translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-540 <FED>

A/Cross-references: UNIPROT:O48683; EMBL:AC002396; NID:g2749918; PIDN:AAC00577.1; PID:g2

C/Genetics:

A/Genes: ATSP:F316.9

A/Map position: 1

A/Introns: 14/3; 281/3; 428/3; 448/2; 483/3; 502/3

C/Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-binc

Query Match 5.3%; Score 93.5; DB 2; Length 540;

Best Local Similarity 27.8%; Pred. No. 6.7; Mismatches 54; Indels 15; Gaps 3;

Matches 32; Conservative 14; Mismatches 54; Indels 15; Gaps 3;

12 IGDGKQTLVLPNG--VNPTNGVSLQAGAVPALERKRVTVSVQSPRKN-KYQV 67

255 VKKEKPPNLIKNDGNVRINPTRGSLKPNQVGKPEPTNTVTSRKTPPEKMNMMKATK 314

68 KIQNPACTANGSCDPSVTRQAVDYTFSTQYSDERAPVTEIAALLASPL 122

315 KPAAPMSKSPQGFAPVRYKPAPTYKLSLSTSHSLKKEK-----VAPPL 358

RESULT 11

A36911 glutamine synthetase I - Pyrococcus woesei

C/Species: Pyrococcus woesei

C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A36911

R/Tiboni, O.; Cammarano, P.; Sanangelanton, A.M.

J. Bacteriol. 175, 2961-2969, 1993

A/Title: Cloning and sequencing of the gene encoding glutamine synthetase I from the arch

etase I sequences.

A/Reference number: A36911; PMID:9325940; PMID:8098326

A/Accession: A36911

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-439 <TIB>

A/Cross-references: UNIPROT:P36687; GB:X60161; NID:g311383; PIDN:CAA42730.1; PID:g311384

A/Note: sequence extracted from NCBI backbone (NCBI:131878, NCBI:P.131879)

C/Superfamily: glutamate-aminonia ligase

Query Match 5.3%; Score 93; DB 2; Length 439;

Best Local Similarity 23.2%; Pred. No. 5.6; Mismatches 44; Indels 62; Gaps 8;

Matches 39; Conservative 23; Mismatches 44; Indels 62; Gaps 8;

131 PAWVTLIINGSGSGKPDVIPPDP-----PPTGKTCPPAIWSLEVEY 179

308 PAFW-----GKARIEIRCPDPSANPFARAAVAKAGLDGKKHIDPFA-VYENNYE 359

180 PPTKN-----PPIYNAVELQPREVDALKDILG-----NTKRWDSRLSYTT 224

360 MSEKKEKKEIGETLPSTLGEA--LEELKDKVYKEMALGAYKNFINYKKEWESYLEY- 416

225 FRGCRNGYIDDATYLATDQMRDQKDIRGKKGAGNTERFTYL 272

417 -----EKKHMPKOTKVTEN-ELERYPL 439

RESULT 12

A40213 optic lobe development omb protein - fruit fly (Drosophila melanogaster).

N/Alternate names: omb protein

C/Species: Drosophila melanogaster

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: A40213; S34827

R/Flugfelder, G.O.; Roth, H.; Peock, B.; Kercher, S.; Schwarz, H.; Jonschker, B.; Heise

Proc. Natl. Acad. Sci. U.S.A. 89, 1199-1203, 1992

A/Title: The lethal(1)optomotor-blind gene of Drosophila melanogaster is a major organize

A/Reference number: A40213; PMID:92159016; PMID:1741374

A/Accession: A40213

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-974 <PFL>

A/Cross-references: UNIPROT:Q24432; GB:M81796; NID:g158018; PIDN:AAA28736.1; PID:g158019

A/Note: sequence extracted from NCBI backbone (NCBI:P.82056)

R/Peock, B.; Balle, J.; Flugfelder, G.O.

Mol. Gen. Genet. 239, 325-332, 1993

A/Title: Transcript identification in the optomotor-blind locus of Drosophila melanogaster

A/Reference number: S34827; PMID:93261414; PMID:8492800

DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A:Reference number: A99629; PMID:21156231; PMID:11258796
A:Accession: E90696
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1461 <HAY>
A:Cross-references: UNIPROT:O6XD19; GB:BA000007; PIDD:BAR33964.1; PIDD:G13359999; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
A:Genetics:
A:Gene: Ecs0541

Query Match 5.2%; Score 91.5; DB 2; Length 1461;

Best Local Similarity 21.1%; Pred. No. 36;

Matches 72; Conservative 40; Mismatches 144; Indels 85; Gaps 14;

```
QY 13 GADGKOTLVNPRGVPNTNGVSLSQAGVPALEK---RVTVSVSQP-----SRNRK 61
Db 856 GNTGSOSLTVTVTAPLIGINSIAGDDVINASEKGADLQITGTSQDPVNTAITVTIANGQ 915
QY 62 NYKVVQKIGN-----PFACTANGSCDPSVTRQAYADVTFSFTQYSTDEBRAFVTELA 114
Db 916 NYTTTDSAGNMSVTVPASAVTALGQANYTVT---AAVTSDIGNSATASHNVLDSPALP 971
QY 115 ALIASPLIDALDOLNPAYWTLIIAGSGSGSKPDPIPPIDPPPGTKYTCPPAIWSL 174
Db 972 GVTINPVATDDIINAAEAGVAGTISGVTGAEDGT-----VTITLGNVTYATVG---- 1022
QY 175 EEVYEPPTKRPPWPIYNNAVELQPREFDVALKDI--LGNTKMRDWSRLSYTTFRCGRNG 232
Db 1023 -----SNLTWSV-----DVPADDIQALGN--GDLTVNASVTNONGNTGSG 1060
QY 233 ----YIDLATYATLATQAMRDQKVDIRE-----GKKPG-----AFGNIERFIY 271
Db 1061 TRDITIDANPGIRVDTVAGDDVNVIIIEGQALVTGSSGLAESTPLTYTINNVE---Y 1117
QY 272 LKSINAYCSLS-----DIAAYHADGVIVGFWRDPSSGAI 306
Db 1118 TTRAVQADGWSVGVTAAQVSAMPAGTVNTIIVSGESSAIGNSV 1158
```

Search completed: January 4, 2005, 09:17:28
Job time : 21.8066 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 90.3943 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-4

Perfect score: 1749
Sequence: 1 MAKETVTLGNIGKDGKQTL.....FTKPKTKPCIPQAVIVPRA 329

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_02:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1749	100.0	329	2	Q8LTEL
2	1749	100.0	329	2	AAA16663
3	1362	77.9	329	2	O64307
4	1343	76.8	329	2	O64303
5	983	56.2	331	1	VA1_BREP
6	897.5	51.3	330	2	O64310
7	668	38.2	133	2	AAA33126
8	663	37.9	132	1	COAT_BPOBE
9	577	33.0	133	2	O9TOR9
10	557	31.8	133	2	O9TOR8
11	542.5	31.0	132	1	COAT_BPSP
12	506.5	29.0	132	2	O9TOR8
13	118	6.7	329	2	O66157
14	117	6.7	131	1	COAT_BPPRR
15	113.5	6.5	409	2	O97YZ7
16	107	6.1	353	2	O919P4
17	106	6.1	473	2	O8VDC2
18	106	6.1	903	2	O86728
19	104	5.9	873	2	O6TDS3
20	104	5.9	803	2	AAQ9280
21	100	5.7	955	2	O92625
22	100	5.7	955	2	O7CRG9
23	98	5.6	785	2	O8ZTV7
24	98	5.6	1197	2	O6P9Q4
25	98	5.6	1197	2	O8BMR2
26	98	5.6	1197	2	AAH60654
27	97	5.5	1426	2	O9X3P6
28	95.5	5.5	1326	2	O9HYU6
29	95.5	5.5	1365	2	O37174
30	95	5.4	1365	2	O65005
31	94.5	5.4	530	1	TACY_LISSE

32	94.5	5.4	530	2	AA97361	AA97361 listeria
33	94.5	5.4	810	2	O944W5	O944W5 oryza sativ
34	94	5.4	501	1	GDPS_HUMAN	P43026 homo sapien
35	94	5.4	905	1	VP3_AHSV4	P32509 african hor
36	93.5	5.3	540	2	O48683	O48683 arabidopsi
37	93.5	5.3	552	2	O8X045	O8X045 neurospora
38	93.5	5.3	978	2	O7T0G3	O7T0G3 mus musculu
39	93.5	5.3	1249	2	O8CHH2	O8CHH2 mus musculu
40	93	5.3	439	1	GLNA_PYRPU	O05907 pyrococcus
41	93	5.3	439	1	GLNA_PYRMO	P36687 pyrococcus
42	93	5.3	972	1	OMB_DROME	O24432 drosophila
43	93	5.3	4382	2	O6TH39	O6TH39 sars corona
44	93	5.3	4382	2	O6TH47	O6TH47 sars corona
45	93	5.3	4382	2	O6R7Y7	O6R7Y7 sars corona

ALIGNMENTS

RESULT 1									
ID	Q8LTEL	PRELIMINARY;	PRT;	329	AA.				
AC	Q8LTEL								
DT	01-OCT-2002 (TrEMBLrel. 22, Created)								
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)								
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)								
DE	A1 read-through protein (A1 protein).								
OS	Bacteriophage Q-beta.								
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;								
OC	Allolevivirus.								
OX	NCBI_Taxid=12009;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	PubMed=14667253;								
RA	Bacher J.M., Bull J.J., Ellington A.D.;								
RT	"Evolution of phage with chemically ambiguous proteomes.";								
RL	BMC Evol. Biol. 3:24-24(2003).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=94109687; PubMed=7506687;								
RA	Kozlovskaya T.M., Cielens I., Dreilima D., Dislers A., Baumanis V.,								
RT	Ose V., Pumpens P.;								
RL	"Recombinant RNA phage Q beta capsid particles synthesized and self-								
DR	assembled in Escherichia coli.";								
DR	Gene 137:133-137(1993).								
DR	EMBL; AY099114; AAM33127.1; -.								
DR	EMBL; M99039; AAA16663.1; -.								
DR	HSSP; P03615; 10BE.								
DR	GO; GO:0019028; C:Viral capsid; IEA.								
DR	GO; GO:0005198; F:Structural molecule activity; IEA.								
DR	InterPro; IPR002703; Levi_coat.								
DR	InterPro; IPR000504; RNA_rec_mot.								
DR	Pfam; PF01819; Levi_coat; 1.								
DR	PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.								
SQ	SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;								
Query Match 100.0%; Score 1749; DB 2; Length 329;									
Best Local Similarity 100.0%; Pred. No. 4.6e-133;									
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MAKETVTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSOPSRNR	60						
DB	1	MAKETVTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGVPALEKRVTVSVSOPSRNR	60						
QY	61	KNYKVQVKQNPACTANGSCDPSVTRQAVYADVTSFTQYSTDERAFVRELAALLASP	120						
DB	61	KNYKVQVKQNPACTANGSCDPSVTRQAVYADVTSFTQYSTDERAFVRELAALLASP	120						
QY	121	LILDAIDQNPAYWTLTLAGGSGSKPDVPIIDPEIDPPGKXTCPFAISLEVEYEP	180						
DB	121	LILDAIDQNPAYWTLTLAGGSGSKPDVPIIDPEIDPPGKXTCPFAISLEVEYEP	180						
QY	181	PTKRPWPPIYNAVELQPREFDVALKDLGNTKMRDMSRLSYTTFRCGRNGYIDLDATY	240						

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Db      181 PTKRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSTYTFRGCGNGYIDLDATY 240
Qy      241 LATDQMRDQKDIIRGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
Db      241 LATDQMRDQKDIIRGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
Qy      301 SSGGAIIPDFTKPKTCPIQAVIVPRA 329
Db      301 SSGGAIIPDFTKPKTCPIQAVIVPRA 329

```

RESULT 2

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AAAA6663 PRELIMINARY; PRT; 329 AA.
AC 064307;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; Pubmed=7506687;
RA Kozlovskaya T.M., Clemons I., Dreilima D., Dislers A., Baumanie V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137 (1993).
DR EMBL: M99039; AAA16663.1;
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

```

```

Query Match      100.0%; Score 1749; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.6e-133;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MAKLEVTTLGNIGDGKQTLVLPNGVNPNGVASTSQAGVPALEKRVTVSVQPSRNR 60
Db      1 MAKLEVTTLGNIGDGKQTLVLPNGVNPNGVASTSQAGVPALEKRVTVSVQPSRNR 60
Qy      61 KNYKQVKIQNTPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALASP 120
Db      61 KNYKQVKIQNTPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALASP 120
Qy      121 LLIDAIQQLNPAYWTLIIAGGSGSKDPVYIPDPIDPPPGTGKTCPPAIVSLSEYEP 180
Db      121 LLIDAIQQLNPAYWTLIIAGGSGSKDPVYIPDPIDPPPGTGKTCPPAIVSLSEYEP 180
Qy      181 PTKRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSTYTFRGCGNGYIDLDATY 240
Db      181 PTKRPMPIYNAVELQPREFDVALKDLGNTKMRDMSLSTYTFRGCGNGYIDLDATY 240
Qy      241 LATDQMRDQKDIIRGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
Db      241 LATDQMRDQKDIIRGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWRDP 300
Qy      301 SSGGAIIPDFTKPKTCPIQAVIVPRA 329
Db      301 SSGGAIIPDFTKPKTCPIQAVIVPRA 329

```

RESULT 3

```

064307 PRELIMINARY; PRT; 329 AA.
AC 064307;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage X1.

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```

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; Pubmed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; Pubmed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF059242; AAC14700.1; -.
DR HSSP: P03615; 10BR.
DR GO: 0019028; C: viral capsid; IEA.
DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR002703; Lev1_coat.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF01819; Lev1_coat; 1.
DR PROSITE: PS00030; RRM_RNP_1; UNKOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372BDD5DD852F15 CRC64;

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Query Match      77.9%; Score 1362; DB 2; Length 329;
Best Local Similarity 76.4%; Pred. No. 9.1e-102;
Matches 253; Conservative 26; Mismatches 46; Indels 6; Gaps 2;

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Qy      1 MAKLEVTTLGNIGDGKQTLVLPNGVNPNGVASTSQAGVPALEKRVTVSVQPSRNR 60
Db      1 MAKLEVTTLGNIGDGKQTLVLPNGVNPNGVASTSQAGVPALEKRVTVSVQPSRNR 60
Qy      61 KNYKQVKIQNTPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALASP 120
Db      61 KNYKQVKIQNTPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALASP 120
Qy      121 LLIDAIQQLNPAYWTLIIAGGSGSKDPVYIPDPIDPPPGTGKTCPPAIVSLSEYEP 177
Db      121 LLIDAIQQLNPAYWTLIIAGGSGSKDPVYIPDPIDPPPGTGKTCPPAIVSLSEYEP 177
Qy      178 YEBPTKRPMPYINAVELQPREFDVALKDLGNTKMRDMSLSTYTFRGCGNGYIDLD 237
Db      178 YEBPTKRPMPYINAVELQPREFDVALKDLGNTKMRDMSLSTYTFRGCGNGYIDLD 237
Qy      238 ATSLMDVLTSSKYLVRGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWR 297
Db      238 ATSLMDVLTSSKYLVRGKKPGAFGNIERFIYLSINAYCSLSIDIAAYHADGVIYGFWR 297
Qy      298 RDPSSGAIIPDFTKPKTCPIQAVIVPRA 328
Db      298 RDPSSGAIIPDFTKPKTCPIQAVIVPRA 328

```

RESULT 4

```

064303 PRELIMINARY; PRT; 329 AA.
AC 064303;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
NCBI_TaxID=74336;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE-95239761; PubMed-7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917 (1995).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-96190948; PubMed-8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
J. Mol. Biol. 256:8-19 (1996).
RN
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AR052431; AAC0651.1; -.
DR HSP: P03615; 1QBE.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR002703; Levi_coat.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF01819; Levi_coat; 1.
DR PROSITE: PS00030; RNP_1; UNKNOWN_1.
SQ SEQUENCE 329 AA; 35893 MW; 3E33CD821EB625F4 CRC64;

Query Match 76.8%; Score 1343; DB 2; Length 329;
Best Local Similarity 76.8%; Pred. No. 3.1e-100; Matches 252; Conservative 21; Mismatches 54; Indels 2; Gaps 2;

QY 1 MAKLEVTLTGNGKQKQTLVNPNGVPTNGVSLSQAGVPALEKRYTVSVSOPSRNR 60
DB 1 MAKLGVTITSGKGGKQDVTLLNPRGVNPTNGVSLSEAGVPALEKRYTVISVOPSRNR 60
QY 61 KNYKQVKIQNPACTCANGSCDPSVTRQAYADVTSTFTQSTDEBERAFVTELAALASP 120
DB 61 KNYKQVKIQNPACTCANGSCDPSVTRQAYADVTSTFTQSTDEBERAFVTELAALASP 120
QY 121 LVIDAIDQNPAYWTLTIAGGGSGSKDP-VIPDPIDPPPGTKYTCFPAIWSLEAYE 179
DB 121 LVIDAIDQNPAYWTLTIAGGGSGSKDP-VIPDPIDPPPGTKYTCFPAIWSLEAYE 179
QY 180 PPTKRPMPFIYNAVELQPREFVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLDAI 239
DB 180 AANSSSWIYNAVELSPNFDALDGLGNTMRDMSRLSTYTRGCRGNGYIDLDAI 239
QY 240 YLATDQAMDQKXIDIREGKPGAFGNIERFIYKLSINAYCSLSIDIAAHADGVTVGFWRD 299
DB 240 SLMKDEYLTSSKYLVEGRKPGVFGNIEFVYKLSINAYCSLSIDIAHRTDGVTVGFWRD 299
QY 300 PSSGGAIPDPFTKEDTKCPICQAVIVPR 328
DB 300 PSSGGAIPDPFTKEDTKCPICQAVIVPR 328

RESULT 5
VAL_BPSP STANDARD; PRT; 331 AA.
AC P09677;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Readthrough protein A1 [Contains: Coat protein].
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alilevirivirus.
OX NCBI_TaxID=12027;
RN
RP SEQUENCE FROM N.A.
RA MEDLINE-88289362; PubMed-3399390;
RA Hirashina A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA

RT coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221 (1988).
CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
protein sequence.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X07489; CAB37299.1; -.
DR PIR: S01964; S01964.
DR HSP: P03615; 1QBE.
DR InterPro: IPR002703; Levi_coat.
DR Pfam: PF01819; Levi_coat; 1.
KW Coat protein.
FT CHAIN 1 132 Coat protein.
FT FT 1 331 Readthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A6642B52C6582 CRC64;

Query Match 56.2%; Score 983; DB 1; Length 331;
Best Local Similarity 58.5%; Pred. No. 4.1e-71; Matches 197; Conservative 45; Mismatches 77; Indels 18; Gaps 9;

QY 1 MAKLEVTLTGNGKQKQTLVNPNGVPTNGVSLSQAGVPALEKRYTVSVSOPSRNR 60
DB 1 MAKLGVTITSGKGGKQDVTLLNPRGVNPTNGVSLSEAGVPALEKRYTVISVOPSRNR 60
QY 61 KNYKQVKIQNPACTCANGSCDPSVTRQAYADVTSTFTQSTDEBERAFVTELAALASP 120
DB 61 KNYKQVKIQNPACTCANGSCDPSVTRQAYADVTSTFTQSTDEBERAFVTELAALASP 119
QY 121 LVIDAIDQNPAYWTLTIAGGGSGSKDP-VIPDPIDPPPGTKYTCFPAIWSLEAYE 175
DB 121 LVIDAIDQNPAYWTLTIAGGGSGSKDP-VIPDPIDPPPGTKYTCFPAIWSLEAYE 177
QY 176 EYEPPTKRPMPFIYNAVELQPREFVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLDAI 232
DB 176 EYEPPTKRPMPFIYNAVELQPREFVALKDLGNTKMRDMSRLSTYTRGCRGNGYIDLDAI 236
QY 233 YIDLATYATQAMDQKXIDIREGKPGAFGNIERFIYKLSINAYCSLSIDIAAHADGVTVGFWRD 290
DB 233 YIDLATYATQAMDQKXIDIREGKPGAFGNIERFIYKLSINAYCSLSIDIAAHADGVTVGFWRD 293
QY 291 GVIVGFWRDPSSGGAIPDPFTKEDTKCPICQAVIVPR 327
DB 291 GVIVGFWRDPSSGGAIPDPFTKEDTKCPICQAVIVPR 329

RESULT 6
ID 064310 PRELIMINARY; PRT; 330 AA.
AC 064310;
DT 01-AUG-1998 (TREMREL. 07, Created)
DT 01-AUG-1998 (TREMREL. 07, Last sequence update)
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alilevirivirus.
OX NCBI_TaxID=75725;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-95239761; PubMed-7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917 (1995).
RN

RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -.
 DR HSSP; P03615; 1QBE.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1 coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 330 AA; 36175 MW; 961855F408334410 CRC64;

Query Match 51.3%; Score 897.5; DB 2; Length 330;
 Best Local Similarity 54.5%; Pred. No. 3.3e-64;
 Matches 181; Conservative 46; Mismatches 96; Indels 9; Gaps 7;

QY 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSQPSRR 60
 DB 1 MAKLNVTTLGIGKAGNQTLLPFGVPTNGVASLSQAGAVPALEKRVTVSVSQPSRR 60
 QY 61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVFSTQYSTDEBERAFVETLALLASP 120
 DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVFSTQYSTDEBERAFVETLALLASP 120
 QY 61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVFSTQYSTDEBERAFVETLALLASP 120
 DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVFSTQYSTDEBERAFVETLALLASP 120
 QY 121 LLIDAIDQINPAYW-TLLTAGGGSGSKPDVITDPP-IDPPGTGKYTCFPAIWSLEEVY 178
 DB 120 LLIDAIDQINPAYW-TLLTAGGGSGSKPDVITDPP-IDPPGTGKYTCFPAIWSLEEVY 178
 QY 179 EPTTKNRPMPIYNAVELQPREFDVALKDLGNTKMDWDSRLS---YTFRGCRNGGYID 235
 DB 180 -TEAKDQACALVAGSBALEVFYALBEDFLGNFPMNMDRLSKYDIEHRRCRKNGGYD 238
 QY 236 LDATYATDQAMDQKYDIRGKKPGAFGNTERFYIKSLINAYCSLDIAHYADGVYIG 295
 DB 239 LDASVWQSDRYVLSGAYDVVKMPGTFDPSRYTLHMD-GIYVDLAEVYAYRSYGVWIG 297
 QY 296 FWRDPSSGAIIPDFTKEDTKCPIQAVITVP 327
 DB 298 FWTDD-SKSPQLPTDFTFRHNCPCVQTVIIP 328

RESULT 7

AAM33126 PRELIMINARY; PRT; 133 AA.
 AC AAM33126;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Coat protein.
 OS Bacteriophage Q-beta.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviruses; Alloviridae subgroup III.
 OX NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Becher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes.";
 RL BMC Evol. Biol. 3:24-24(2003).
 DR EMBL; AY099114; AAM33126.1; -.
 KW Coat protein.
 SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 38.2%; Score 668; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 3.9e-46;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSQPSRR 60
 DB 1 MAKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSQPSRR 60
 QY 61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVFSTQYSTDEBERAFVETLALLASP 120
 DB 61 KNYKVQVKIQNPACTANGSCDPSVTRQAVADVFSTQYSTDEBERAFVETLALLASP 120
 QY 121 LLIDAIDQINPAY 133
 DB 121 LLIDAIDQINPAY 133

RESULT 8

COAT_PROBE
 ID COAT_PROBE STANDARD; PRT; 132 AA.
 AC P03615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Coat protein.
 OS Bacteriophage Q-beta.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviruses.
 OX NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94109687; PubMed=7506687;
 RA Kozlovskaya T.M., Clelens I., Dreilina D., Dislers A., Baumanis V.,
 RA Ose V., Pumpens P.;
 RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
 RT assembled in Escherichia coli.";
 RL Gene 137:133-137(1993).
 RN [2]
 RP SEQUENCE OF 1-80 FROM N.A.
 RX MEDLINE=79048469; PubMed=361741;
 RA Escarim C., Sastry P.A., Billeter M.A.;
 RT "Determination of the first half of the coat protein cistron of
 RT bacteriophage Q-beta as an application of a mapping procedure for RNA
 RT fragments.";
 RL J. Biol. Chem. 253:8390-8399(1978).
 RN [3]
 RP REVISIONS TO 1-60.
 RX MEDLINE=7118579; PubMed=838709;
 RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
 RT "Revised amino acid sequence of Qbeta coat protein between positions 1
 RT and 60.";
 RL J. Biol. Chem. 252:990-993(1977).
 RN [4]
 RP SEQUENCE.
 RX MEDLINE=71288580; PubMed=5570434;
 RA Watta T., Konigsberg W.;
 RT "The amino acid sequence of the Q-beta coat protein.";
 RL J. Biol. Chem. 246:5003-5024(1971).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
 RX MEDLINE=96347354; PubMed=8736553;
 RA Golmohammadi R., Fridborg K., Bundale M., Valegard K., Liljas L.;
 RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
 RL Structure 4:543-554(1996).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 CC -----
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 CC -----
 DR EMBL; M99039; AAA16662.1; -.

DR EMBL; V00643; CAA23992.1; -.
 DR PIR; A92240; VCBPQB.
 DR PDB; 1QBE; X-ray; A/B/C=1-132.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat.1.
 DR 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
 KW INIT_MER 0
 FT CONFLICT 22 22 N -> D (in Ref. 4).
 FT CONFLICT 56 56 Missing (in Ref. 4).
 FT TURN 6 9
 FT TURN 13 14
 FT TURN 18 27
 FT TURN 28 31
 FT STRAND 32 36
 FT STRAND 42 44
 FT STRAND 47 53
 FT STRAND 56 56
 FT TURN 57 58
 FT STRAND 59 59
 FT STRAND 62 74
 FT STRAND 83 96
 FT TURN 98 99
 FT HELIX 102 117
 FT HELIX 119 126
 FT TURN 127 127
 SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 37.9%; Score 663; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 9.7e-46;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQSPSRNR 61
 DB 1 AKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQSPSRNR 60
 QY 62 NKVKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBRATVTELAALIASPL 121
 DB 61 NKVKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBRATVTELAALIASPL 120
 QY 122 LIDAIIDQINPAY 133
 DB 121 LIDAIIDQINPAY 132

RESULT 9
 Q9TOR9 PRELIMINARY; PRT; 133 AA.

AC Q9TOR9; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Major coat protein.
 OS Enterobacteria phage Mx1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC NCBI_TaxID=75723;
 OC 1101levivirus.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RT RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;

RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059242; AAC14699.1; -.
 DR HSSP; P03615; 1QBE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat.1.
 KW Coat protein.
 SQ SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;

Query Match 33.0%; Score 577; DB 2; Length 133;
 Best Local Similarity 84.2%; Pred. No. 8.8e-39;
 Matches 112; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQSPSRNR 60
 DB 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQSPSRNR 60
 QY 61 NKVKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBRATVTELAALIASPL 120
 DB 61 NKVKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQYSTDEBRATVTELAALIASPL 120
 QY 121 LIDAIIDQINPAY 133
 DB 121 LIDAIIDQINPAY 132

RESULT 10
 Q9TOR9 PRELIMINARY; PRT; 133 AA.

AC Q9TOR9; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Coat protein.
 OS Bacteriophage M11.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC 1101levivirus.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RT RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 RT Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
 RT Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF052431; AAC06250.1; -.
 DR HSSP; P03615; 1QBE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR002703; Levi_coat.
 DR Pfam; PF01819; Levi_coat.1.
 KW Coat protein.
 SQ SEQUENCE 133 AA; 14198 MW; 098722B3C6C3A255 CRC64;

Query Match 31.8%; Score 557; DB 2; Length 133;
 Best Local Similarity 81.2%; Pred. No. 3.7e-37;
 Matches 108; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQSPSRNR 60
 DB 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVSLSQAGVPALEKRVTVSVQSPSRNR 60

```

QY 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELTALLASP 120
DB 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELTALLASP 120
QY 121 LVIDAIDQNLNPAY 133
DB 121 LVIDAIDQNLNPAY 133

RESULT 11
COAT_BPSP STANDARD; PRT; 132 AA.
ID COAT_BPSP
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altolievivirus.
NCBI_TaxID=12027;
RX MEDLINE=88289362; PubMed=3399390;
RA MEDLINE=88289362; PubMed=3399390;
RT Hiraehina A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -I- FUNCTION: Forms the phage shell; binds to the phage RNA.
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CC -----
DR EMBL; X07489; CA13074.1; -.
DR HSSP; P03615; IOBE.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KM Coat protein; RNA-binding.
SQ SEQUENCE 132 AA; 14129 MW; 50B1B6CC6AF0A254 CRC64;

Query Match 31.0%; Score 542.5; DB 1; Length 132;
Best Local Similarity 79.7%; Pred. No. 5,4e-36;
Matches 106; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVQSPSRR 60
DB 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVQSPSRR 60
QY 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELTALLASP 120
DB 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELTALLASP 120
QY 121 LVIDAIDQNLNPAY 133
DB 121 LVIDAIDQNLNPAY 133

RESULT 12
Q9TOR8 PRELIMINARY; PRT; 132 AA.
ID Q9TOR8
AC Q9TOR8;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NU95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

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OC Altolievivirus.
OX NCBI_TaxID=75725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059243; AAC14703.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KM Coat protein.
SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 29.0%; Score 506.5; DB 2; Length 132;
Best Local Similarity 75.9%; Pred. No. 4,4e-33;
Matches 101; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVQSPSRR 60
DB 1 MAKLETVTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALEKRVTVSVQSPSRR 60
QY 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELTALLASP 120
DB 61 KNYKVQVQKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDERAFVTELTALLASP 120
QY 121 LVIDAIDQNLNPAY 133
DB 121 LVIDAIDQNLNPAY 133

RESULT 13
O66157 PRELIMINARY; PRT; 329 AA.
ID O66157
AC O66157;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Deduced dNDP-hexose 4,6-dehydratase.
GN Name=kaad;
OS Streptomyces kasugaensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1946;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M338-M1;
RX MEDLINE=98250958; PubMed=9589071;
RA Ikono S., Tsuji T., Higashide K., Kinoshita N., Hamada M., Hori M.;
RT "A 7.6 kb DNA region from Streptomyces kasugaensis M338-M1 includes
RT some genes responsible for kasugamycin biosynthesis.";
RL J. Antibiot. 51:341-352(1998).
DR EMBL; AB005901; BA25656.1; -.
DR HSSP; P27830; IBXK.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0016857; P:carboxylate metabolism; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.

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DR InterPro; IPR001509; Epimerase_Dh.
 DR InterPro; IPR008089; Nuc_sugar_epim.
 DR Pfam; PF01370; Epimerase; 1.
 DR PRINTS; PRO1713; NUCEPIMERASE.
 SQ SEQUENCE 329 AA; 35600 MW; 58A0D0354BD36FF4 CRC64;

Query Match 6.7%; Score 118; DB 2; Length 329;
 Best Local Similarity 26.0%; Pred. No. 0.36;
 Matches 52; Conservative 29; Mismatches 91; Indels 28; Gaps 8;

QY 16 GROTIVLNRGVNPNGVSLQAGV-VALEKRVTVSVQSPSRNKNK----- 64
 DB 10 GQVLTGADFTGSHLTETLVSRGARVAVVR--VSAQVTHRLNLAAITDALERV 67
 QY 65 VQVKIQNPACTANGSCDPSVTRQAVADYVTFSTQYSTDERRAFVTELAALIASPLID 124
 DB 68 VAVDLAEPFAVAVVGLLEADTWFLHAA---AVPMSLDQPADVATVNMSTLH---VLL 121
 QY 125 AIDQINPAYWTLILAGGSGSKPDPIVPPPIDP--PQTKYKTCFPAIWSLEEVE-PP 181
 DB 122 AAQOQOPALILVTSSEVVGSDPDAITEHHPLEPATPVAAKVACDRLAMSWHHTYGLPL 181
 QY 182 TKNRPW-----PIYNAVEL 195
 DB 182 TIVRPENSTYGRHVVDAPVL 201

RESULT 14
 COAT_BPPRR STANDARD; PRT; 131 AA.

AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein. PRR1.
 OS Bacteriophage PRR1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC unclassified Leviviridae.
 OC NCBI_TaxId=12024;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhaese P., Vandekerckhove J., van Montagu M.,
 RT "The primary structure of the coat protein of the broad-host-range RNA
 RT bacteriophage PRR1."
 RL Eur. J. Biochem. 94:375-386(1979).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR PIR; A04225; VCBPPI.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KM Coat protein; direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7E639E1E50FC12 CRC64;

Query Match 6.7%; Score 117; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.14;
 Matches 42; Conservative 15; Mismatches 57; Indels 16; Gaps 5;

QY 18 QTLVNLPRGVNPT-----NGVASLSQAGAVPALKRTVSVSQSPSRNKNKVV 67
 DB 4 QNLVNLKDRATPNDHTFVRDIRDNGVAVESITGVPIGSRFTISLRKTSNGR--YKSTL 61
 QY 68 KIQNPFT--ACTANGSCDPSVTRQAVADYVTFSTQYSTDERR-AFVTELAALIASPLI- 123
 DB 62 KLVAVVVGSGQTVNGVITPVVATSVTVVDPDARSTTKERNKPFVGMIDALKADLMVH 121
 QY 124 DAIDQINPAY 133
 DB 122 DTIVNLQGVY 131

RESULT 15
 Q97Y27 PRELIMINARY; PRT; 409 AA.

AC Q97Y27;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedAccession=SS01152;
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxId=2287;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=ATCC 35092; PubMed=1142726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA De Moore M.J., Chan-Weher C.C.-Y., Clausen I.G., Cuttis B.A.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Thieriault C., Tolstrup N.,
 RA Charlebois R.L., Doocille W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006731; AKK41403.1; --
 DR PIR; D90268; D90268.
 DR InterPro; IPR002510; Peptidase_U62.
 DR Pfam; PF01523; Pmba_T1D; 1.

DR Pfam; PF01523; Pmba_T1D; 1.
 SQ Complete proteome; Hypothetical protein.
 SQ SEQUENCE 409 AA; 46122 MW; B5AB9BC6831AA522 CRC64;

Query Match 6.5%; Score 113.5; DB 2; Length 409;
 Best Local Similarity 23.0%; Pred. No. 1.1;
 Matches 62; Conservative 36; Mismatches 99; Indels 73; Gaps 13;

QY 89 AYADVTFTQYSTDERRAFVTELAAL-----LASPL-----LIDALQINP 131
 DB 160 AFSSTSFSSQYKDSIKKA--NELASTGKYEITEGKDVILSLVMGNLMEVARMAS 216
 QY 132 AY-----WTLILAGGSGSKPDPIVPPPIDP-----PQT-----GKYTCPF 169
 DB 217 GYAIMSGSMLEKPKGKAGSDKFTLDPKEDRPNSMGFPDDEGTFYNNKAIENGVFTTFL 276
 QY 170 AIMSLEEVE--PTNNRPPIYNAVELQPREPVALKDLG-----NTKWRDMSRLSY 222
 DB 277 LNNELSNVPEKLPSTGNAGIYPTANMLEVKGEDTSFESLISGNVVFINNVM-----Y 328
 QY 223 TTFRCGRNGYIDLATYIATDQAMRDQKTIIRBKGKRGAFENIERFIYLSKINAYCSLS 282
 DB 329 TRFQ-----NYAEGDFSTVA-----RDAVVVVRNNGNPVGIVGRVRIADNLKRI-----LK 373
 QY 283 DIAAHADGVIVGFWRPDSGGAIPDPFTK 312
 DB 374 NIVELSRERYSVRMWDAPMQ--GVYYPALVK 402

Search completed: January 4, 2005, 09:16:14
 Job time : 92.3943 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.88938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663
Sequence: 1 AKLETVTLGNGKDGKQTLV.....AALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	132	1 VCBP0B	coat protein - pha
2	537.5	81.1	331	2 S01964	readthrough protei
3	117	17.6	131	1 VCBPPI	coat protein - pha
4	94.5	14.3	530	2 S22340	beeligeritolysin -
5	89.5	14.1	540	2 T00646	hypothetical prote
6	89.5	13.5	529	2 S24231	listeriolysin O pr
7	89.5	13.5	529	2 A43505	listeriolysin O pr
8	89.5	13.5	529	2 AC1100	listeriolysin O pr
9	81	12.2	130	1 A46324	coat protein - pha
10	80	12.1	130	1 VCBP0A	coat protein - pha
11	79	11.9	432	2 T31660	hypothetical prote
12	78.5	11.8	528	2 S22341	ivanolysin precurs
13	78.5	11.8	1502	1 R8YH1	hypothetical prote
14	78	11.8	830	2 S57537	CycI/CYP3 transcri
15	77.5	11.7	136	2 C98221	hypothetical prote
16	77.5	11.7	136	2 A83065	conserved hypotet
17	77.5	11.7	1052	2 C64221	hypothetical 114K
18	77.5	11.7	1861	2 T13845	microtubule-associ
19	76	11.5	282	2 A10186	probable iron-side
20	76	11.5	340	2 S18650	homeotic protein H
21	76	11.5	340	2 A42008	homeotic protein H
22	75.5	11.4	130	1 VCBPFR	coat protein - pha
23	75.5	11.4	161	4 I55480	hypothetical natri
24	75.5	11.4	1097	2 AD2572	hypothetical prote
25	75	11.3	430	2 G88884	protein K09B1.10
26	74.5	11.2	289	2 C70400	ferredoxin oxidore
27	74.5	11.2	520	1 ACMSD1	nicotinic acetylch
28	74.5	11.2	601	2 A55921	serine/threonine k
29	73.5	11.1	129	1 VCBP2	coat protein - pha

30	73.5	11.1	129	1 VCBP2	coat protein - pha
31	73.5	11.1	129	1 VCBP2R	coat protein - pha
32	73.5	11.1	384	2 A45490	neuropeptide Y/pep
33	73.5	11.1	719	2 T39271	conserved hypotet
34	73.5	11.1	2110	2 H96803	unknown protein T5
35	72.5	10.9	458	2 T49114	hypothetical prote
36	72.5	10.9	654	2 S63673	SAC7 protein - yea
37	72	10.9	399	1 A43685	polymerase-associ
38	72	10.9	1461	2 E90696	hypothetical prote
39	72	10.9	1461	2 A85547	hypothetical prote
40	71.5	10.8	191	2 H90078	hypothetical prote
41	71.5	10.8	683	2 A00899	probable exported
42	71	10.7	243	1 VHVUPT	nucleocapsid prote
43	71	10.7	366	2 F70618	probable putaa pro
44	70.5	10.6	130	1 VCBPM2	coat protein [vali
45	70	10.6	376	2 C84316	hypothetical prote

ALIGNMENTS

RESULT 1

VCBP0B
coat protein - phage Q-beta

C/Species: phage Q-beta
C/Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004

A/Accession: A92240; A92221; A92088; A04224

R/Bscarms, C.; Sastry, P.A.; Biller, M.A.

J. Biol. Chem. 253, 8390-8399, 1978

A/Title: Determination of the first half of the coat protein cistron of bacteriophage Qb

A/Reference number: A92240; MUID:79048469; PMID:361741

A/Accession: A92240

A/Molecule type: mRNA

A/Residues: 1-80 <ESC>

A/Cross-references: UNIPROT:P03615

R/Stoll, E.; Wilson, K.J.; Reiser, J.; Weissmann, C.

J. Biol. Chem. 252, 990-993, 1977

A/Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.

A/Reference number: A92221; MUID:77118576; PMID:838709

A/Accession: A92221

A/Molecule type: protein

A/Residues: 1-60 <STO>

R/Malta, T.; Konigsberg, W.

J. Biol. Chem. 246, 5003-5024, 1971

A/Title: The amino acid sequence of the Qbeta coat protein.

A/Reference number: A92088; MUID:71288580; PMID:5570434

A/Molecule type: protein

A/Residues: 1-21, 'D', '23-55, 57-132 <MAI>

C/Superfamily: phage GA coat protein

Query Match 100.0%; Score 663; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.2e-57; Indels 0; Gaps 0;
Matches 132; Conservative 0; Mismatches 0;

QY	1	AKLETVTLGNGKDGKQTLVNPGRVPTNGVASSQAGVPALEKRVTVSVQSPRRK	60
DB	1	AKLETVTLGNGKDGKQTLVNPGRVPTNGVASSQAGVPALEKRVTVSVQSPRRK	60
QY	61	NYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQSYDDEBAFVETELAAALASP	120
DB	61	NYKVQVKIQNPACTANGSCDPSVTRQAYADVTFSFTQSYDDEBAFVETELAAALASP	120
QY	121	LIDALDQNPAY 132	
DB	121	LIDALDQNPAY 132	

RESULT 2
S01964
readthrough protein - phage SP
C/Species: phage SP
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S01964
C:Inokuchi, Y.; Jacobson, A.B.; Hirose, T.; Inayama, S.; Hirashima, A.
Nucleic Acids Res. 16, 6205-6221, 1988
A:Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP
A:Reference number: S01963; MUID:88289362; PMID:3399390
A:Accession: S01964
A:Status: Preliminary
A:Molecule type: genomic RNA
A:Residues: 1-331 <IN>
A:Cross-references: UNIPROT:P09677; EMBL:X07489
A:Note: the authors translated the readthrough stopcodon TGA for residue 133 as TTP
;superfamily: phage GA coat protein

Query Match Similarity	81.1%;	Score 537.5;	DB 2;	length 331;
Best Local Similarity	79.5%;	Pred. NC.6.4e-45;		
Matches	105;	Conservative	12;	Mismatches 14; Indels 1; Gaps 1

QY	1	AKELEVTTLGNIGKDGKQTLVLPNGVNPFTNGVASLSQAGAVPALKEKRTVSVSQPSRRNK	60
Db	2	AKLNGVTLSTKIGKNDQTLTLTPRVNPTNGVASLSQAGAVPALKEKRTVSVSQPSRRNK	61
QY	61	NYKQVKIQNPACTANGSCDPSVTRQAVADYTFSTQYSDDEEPAFYRTIELAALLASPL	120
Db	62	NFKVQIKIQNPACTARD-ACDPVSYRSAPADVTLSTFSTYSYSDDEERALLRTEIAALLADPL	120
QY	121	LIDAIQDQNPAY	132
		:::	
Db	121	IVDAIDQNPAY	132
		:::	

```

RESULT 3
VCBPp1
coat protein - phage PRRI
C:/Species: phage PRRI
C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C/Accession: A04225
R/Dhasee, P.; Vandekerckhove, J.S.; Van Montagu, M.C.
Eur. J. Biochem. 94, 375-386, 1979
A/Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage phi-X174
A/Reference number: A04225; MUID:79148387; PMID:107028
A/Accession: A04225
A/Molecule type: protein
A/Residues: 1-131 <DHA>
A/Cross-references: UNIPROT:P03616
A/Superfamily: phage GA coat protein

```

[illegible]

RESULT 4
S22340
seeligeritolysin - *Listeria seeligeri*
C|Species: *Listeria seeligeri*
C|Date: 22-Nov-1993 #sequence
C|Accession: S22340
R|Haas, A.; Dumbsky, M.; Kretz, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A|Title: Listeriolysin genes: complete sequence of ilo from *Listeria ivanovi* and of lsc
|Reference number: S22340; PMID:92182018; PMID:1543752

A:Accession: S22340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 >HAA>
A:CROSS-references: UNIPROT:P31830, EMBL:X60462, NID:G44144, PIDN:CAA42996.1, PID:G44145
A:Note: the authors translated the codon GCC for residue 287 as Pro.
;Superfamily: dipeptide transport protein

	Query Match	14.3%	Score 94.5;	DB 2,	Length 530;
	Best Local Similarity	25.8%;	Pred. No. 0.23;	Mismatches	7.
	Matches	34;	Conservative	23;	Gaps
Oy	13 KDGKQTLVL--NPFGVNPT-----NGVASLSOAGA-----VPALKEKV	48			
Dd	94 KDGSEYIVVEKKKGKGINNNADISVINASLSTYPGALVKANRELVENQPNTLVFKRDSL	153			
Oy	49 TVSVSQSPERNKNKYVOYKIONPFACTANGSCDPSVTR-----QAYADVTFSSFYQYSTD	102			
Dd	154 TLSDVLPEMTKDKNKIFVK--NPTKSNVNAVNLTVLRWMDKRSKSYENINAKI-DYS--	208			
Oy	103 EERAFVRETELA	114			
Dd	209 DEMAYSESOLTA	220			

RESULT 5
T00646
hypothetical protein F316.9 - *Arabidopsis thaliana*
C|Species: *Arabidopsis thaliana* (mouse-ear cress)
C|Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C|Accession: T00646
R|Fedelespiel, N.A.; Palm, C.U.; Conway, A.B.; Kutz, D.B.; Conway, A.R.; Au, M.; Araujo,
Y.; Vysotskai, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davits, R.W.
submitted to the EMBL Data Library, February 1998
A|Reference number: Z14197
A|Accession: T00646
A|Status: translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-540 <FEED>
A|Cross-references: UNIPROT:Q48683; EMBL:AC002396; NID:g2749918; PIDN:AAC00577.1; PID:g28
C|Genetics:
A|Gene: ATP-F316.9
A|Map position: 1
A|Introns: 14/3, 428/3, 448/2, 483/3, 502/3
A|Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bi-

```

Query Match      14.1%  Score 93.5; DB 2  Length 540;
Best Local Similarity 27.8%  Pred. No. 0.29;
Matches 32; Conservative 14; Mismatches 54; Indels 15; Gaps 3

QY 11 ICKGKQKTLVLPNG---VNPETNGVSLSSQKAGVPALEKKRTVSVSOPSRRKRN-YKQV 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 255 VKKEKKKPLIKKNDNVRINPTFSGLSKKNQVGGKPEKTKYTSRKTPSSKKNKKMKATK 314
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 67 KIQNPCTANGSCDPSYTRQIADVTFSEFYQSTDERAFVETLALLSPLL 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

DB 315 KPAAPMSSSPGGFATPRYKAPPTTSISTSHSLKKK-----VSPLL 358
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 6
S24231
listeriolysin precursor -- *Listeria monocytogenes* (strain 12067)
C:Species: *Listeria monocytogenes*
A:Variety: strain 12067
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S24231
R:Rasmussen, O. F.; Beck, T.; Olsen, J. E.; Dons, L.; Rossen, L.
Infect. Immun. 59, 3945-3951, 1991
A:Title: *Listeria monocytogenes* isolates can be classified into two major types according
A:Reference number: S24230; MUID:92040062; PMID:1537753
A:Accession: S24231
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-529 <RAS>
A:Cross-references: UNIPROT:P13128; EMBL:X60035; NID:g44110; PIDN:CAA42639.1; PID:g44112
A:Experimental source: strain 12067, serotype 4b
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C:Genetics:
A:Gene: hlyA
C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-529/Product: listeriolysin O #status predicted <Mat>
Query Match 13.5%; Score 89.5; DB 2; Length 529;
Best Local Similarity 23.5%; Pred. No. 0.71;
Matches 31; Conservative 23; Mismatches 43; Indels 35; Gaps 5;
QY 13 KDGRKTLV-----NPRGVNPTNGVASLSQGA-----VPALKRV 48
DB 93 KDGEYIVVEKKKKKINONNADIQVNAISSLTFTGALVKANSELVENOPDVLVPRKDSL 152
QY 49 TVSVQPSRRNRKRYQVQKIQNPACTANGSCDPSTVTR-----QAYADVTFSTFOYSTD 102
DB 153 TLTSLDPLGNTQNDKNIIVK--NATKSNVNNAVNTLVERNNEKYAQAYPRVS---AKIDVD 207
QY 103 EERAFVTEFLAA 114
DB 208 DEMAYSESQLIA 219
RESULT 7
A:3505
Listeriolysin O precursor - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 21-Oct-1992 #sequence revision 21-Oct-1992 #text_change 09-Jul-2004
A:Accession: A43505; S05306; A47606; S12400; A61079
R:Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanrey
Interf. Immun. 56, 766-772, 1988
A>Title: Expression in Escherichia coli and sequence analysis of the listeriolysin O det
A:Reference number: A43505; MUID:88153053; PMID:3126142
A:Accession: A43505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <MEN>
A:Cross-references: UNIPROT:P13128; GB:M24199; NID:g149652; PIDN:AAA03018.1; PID:g149653
A>Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R:Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A>Title: Nucleotide sequence of the listeriolysin gene from a Listeria monocytogenes ser
A:Reference number: S05306; MUID:89366684; PMID:2505236
A:Accession: S05306
A:Molecule type: DNA
A:Residues: 1-529 <DOM>
A:Cross-references: EMBL:X15127; NID:g44106; PIDN:CAA33223.1; PID:g44107
A:Experimental source: strain EGD
A>Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R:Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cossart, P.
Interf. Immun. 55, 3225-3227, 1987
A>Title: Identification of the structural gene encoding the SH-activated hemolysin of Li
A:Reference number: A47606; MUID:88057627; PMID:2824384
A:Accession: A47606
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 413-480 <ME2>
A:Cross-references: GB:M29171
R:Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cossart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A>Title: Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtain
A:Reference number: S12400; MUID:91211627; PMID:1965218
A:Accession: S12400
A:Molecule type: DNA
A:Residues: 483-493 <MIC>
A:Experimental source: strain LO28, serotype 1/2c
C:Genetics:
A:Gene: hlyA; hlyA, hlyA

C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-529/Product: listeriolysin O #status predicted <Mat>
Query Match 13.5%; Score 89.5; DB 2; Length 529;
Best Local Similarity 23.5%; Pred. No. 0.71;
Matches 31; Conservative 23; Mismatches 43; Indels 35; Gaps 5;
QY 13 KDGRKTLV-----NPRGVNPTNGVASLSQGA-----VPALKRV 48
DB 93 KDGEYIVVEKKKKKINONNADIQVNAISSLTFTGALVKANSELVENOPDVLVPRKDSL 152
QY 49 TVSVQPSRRNRKRYQVQKIQNPACTANGSCDPSTVTR-----QAYADVTFSTFOYSTD 102
DB 153 TLTSLDPLGNTQNDKNIIVK--NATKSNVNNAVNTLVERNNEKYAQAYPRVS---AKIDVD 207
QY 103 EERAFVTEFLAA 114
DB 208 DEMAYSESQLIA 219
RESULT 8
A:1100
Listeriolysin O precursor [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
A:Accession: AC1100
R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Bagnero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Duesselet, O.; Entian, K.D.; Fath, H.;
D.; Jones, L.M.; Karsel, U.
Science 294, 849-852, 2001
A:Authors: Krefel, J.; Kuhn, M.; Kuntz, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voess, H.; Wehlund,
A>Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <Gla>
A:Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:g16409567; GSPDB:C
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: hly
C:Superfamily: dipeptide transport protein
Query Match 13.5%; Score 89.5; DB 2; Length 529;
Best Local Similarity 23.5%; Pred. No. 0.71;
Matches 31; Conservative 23; Mismatches 43; Indels 35; Gaps 5;
QY 13 KDGRKTLV-----NPRGVNPTNGVASLSQGA-----VPALKRV 48
DB 93 KDGEYIVVEKKKKKINONNADIQVNAISSLTFTGALVKANSELVENOPDVLVPRKDSL 152
QY 49 TVSVQPSRRNRKRYQVQKIQNPACTANGSCDPSTVTR-----QAYADVTFSTFOYSTD 102
DB 153 TLTSLDPLGNTQNDKNIIVK--NATKSNVNNAVNTLVERNNEKYAQAYPRVS---AKIDVD 207
QY 103 EERAFVTEFLAA 114
DB 208 DEMAYSESQLIA 219
RESULT 9
A:6324
coat protein - phage JP34
C:Species: phage JP34
A>Note: host Escherichia coli
C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
A:Accession: A46324
R:Adhin, M.R.; Hirashima, A.; Van Duin, J.
Virology 170, 238-242, 1989
A>Title: Nucleotide sequence from the ssRNA bacteriophage JP34 resolves the discrepancy i

A:Reference number: A46324; MUID:89243181; PMID:2718383
 A:Accession: A46324
 A:Molecule type: genomic RNA
 A:Residues: 1-130 <ADH>
 A:Cross-references: UNIPROT:P34700; GB:J04343; NID:g215076; PIDN:AAA72210.1; PID:g215077
 C:Superfamily: phage GA coat protein
 C:Keywords: coat protein

Query Match 12.2%; Score 81; DB 1; Length 130;
 Best Local Similarity 25.0%; Pred. No. 0.94;
 Matches 35; Conservative 24; Mismatches 61; Indels 20; Gaps 5;

QY 1 AALEVTTLGNIGKDGQTLVLPNGVPTNGVA-----SLSQAGVPALEKRYTVSVSQ 54
 DB 2 AATRSFVLVDNNGTGVTVV---PVSANANGVAEMLSNNSRSGA-----YKVTASRA 50
 QY 55 PARNRNKYKQVYKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVETELAA 114
 DB 51 SGADRRKRTIKLEVPKIVYQVNVGVELPVSAMKAVASIDLTIPFATDDVTVISKSLAG 110
 QY 115 L--LASPLLDIDAIDQNPAY 132
 DB 111 LFKVGNP-IADAISSQSGFY 129

RESULT 10
 VCBPGA
 coat protein - phage GA
 C:Species: phage GA
 A>Note: host Escherichia coli
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29178
 R:Inokuchi, Y.; Takahashi, R.; Hirose, T.; Inayama, S.; Jacobson, A.B.; Hirashima, A.
 J. Biochem. 99, 1169-1180, 1986
 A:Title: The complete nucleotide sequence of the group II RNA coliphage GA.
 A:Reference number: A92000; MUID:86223910; PMID:3711059
 A:Accession: A29178
 A:Molecule type: genomic RNA
 A:Residues: 1-130 <INO>
 A:Cross-references: UNIPROT:P07234; GB:D10027; GB:D00046; GB:X03869; NID:g217784; PIDN:H
 C:Superfamily: phage GA coat protein
 C:Keywords: coat protein

Query Match 12.1%; Score 80; DB 1; Length 130;
 Best Local Similarity 24.3%; Pred. No. 1.2;
 Matches 34; Conservative 25; Mismatches 61; Indels 20; Gaps 5;

QY 1 AALEVTTLGNIGKDGQTLVLPNGVPTNGVA-----SLSQAGVPALEKRYTVSVSQ 54
 DB 2 AATRSFVLVDNNGTGVTVV---PVSANANGVAEMLSNNSRSGA-----YKVTASRA 50
 QY 55 PARNRNKYKQVYKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVETELAA 114
 DB 51 SGADRRKRTIKLEVPKIVYQVNVGVELPVSAMKAVASIDLTIPFATDDVTVISKSLAG 110
 QY 115 L--LASPLLDIDAIDQNPAY 132
 DB 111 LFKVGNP-IADAISSQSGFY 129

RESULT 11
 T3160
 hypothetical protein COS41.6 - sea squirt (Cliona intestinalis)
 C:Species: Cliona intestinalis
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T3160
 R:Bird, A.P.; Clark, V.; Jones, S.J.; Leitegeb, S.; Dobson, R.; Tweedie, S.
 submitted to the EMBL Data Library, December 1996
 A:Reference number: Z21049
 A:Accession: T3160
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-432 <BIR>

A:Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDN:CAB06050
 C:Genetics:
 A:introns: 180/2; 212/1; 229/3

Query Match 11.9%; Score 79; DB 2; Length 432;
 Best Local Similarity 28.3%; Pred. No. 5.9;
 Matches 30; Conservative 15; Mismatches 51; Indels 10; Gaps 5;

QY 4 ETVTLGNIGKDGQTLVLPNGVPTNGVASLSQAGVPALEKRYTVSVSQPSNRKNTK 63
 DB 242 DTSSGEVTKDQPGNLAENP---TPSNAREIQESVASEVLETTVAKSAIQ-EODSAYR 297
 QY 64 VQVKIQNPAC-TANGSCDPSVTRQAVADVTFSTQYSTDEERAFVETELAA 104
 DB 298 KE-NPQNAAPACPNRNGNCVTSNKTSPDSKIEIVNDSDDNTTDD 342

RESULT 12
 S22341
 Ivanolysin precursor - Listeria ivanovii
 C:Species: Listeria ivanovii
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
 C:Accession: S22341; S36683
 R:Haas, A.; Dumbeky, M.; Kreft, J.
 Biochim. Biophys. Acta 1130, 81-84, 1992
 A:Title: Listeriolysin genes: complete sequence of ilo from Listeria ivanovii and of ilo
 A:Reference number: S22340; MUID:92182018; PMID:1543752
 A:Accession: S22341
 A:Molecule type: DNA
 A:Residues: 1-528 <HAS>
 A:Cross-references: UNIPROT:P31831; EMBL:X60461
 A>Note: the authors translated the codon ACA for residue 331 as Val
 R:Kreft, J.
 submitted to the EMBL Data Library, July 1991
 A:Reference number: S36683
 A:Accession: S36683
 A:Molecule type: DNA
 A:Residues: 1-319, 'T', 321-528 <KRB>
 A:Cross-references: EMBL:X60461
 C:Genetics:
 A:Gene: ilo
 C:Superfamily: dipeptide transport protein
 F:1-24/Domains: signal sequence #status predicted <SIG>
 F:25-528/Product: Ivanolysin #status predicted <MAT>

Query Match 11.8%; Score 78.5; DB 2; Length 528;
 Best Local Similarity 22.0%; Pred. No. 8.4;
 Matches 29; Conservative 23; Mismatches 45; Indels 35; Gaps 5;

QY 13 KDGKQTLV-----NPRGVNPTNGVASLSQAGVPALEKRYTVSVSQPSNRKNTK 48
 DB 92 KEGNQYIVVEKKKKKINQNNADIQVINSLASLTYPGALVKANSELVENQDVLVYKRDV 151
 QY 49 TVSVQPSNRKNKYKQVYKIQNPACTANGSCDPSVTR-----QAVADVTFSTQYSTD 102
 DB 152 TLSDLP--GMVNDNEIVQVATKSNINDGVNTLVDRMNNKYSSEYPAIS--AKIDVD 206
 QY 103 EERAFVETELAA 114
 DB 207 QEMAYSESQLVA 218

RESULT 13
 RGSBYH
 CYC1/CYP3 transcription activator - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein 19672.1; protein YLR256w; regulatory protein CYC1, regulatory
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Sep-1991 #sequence_revision 23-Feb-1996 #text_change 12-Nov-1999
 C:Accession: S59400; A13112; S15447; S05804; S15446
 R:Johnson, D.
 submitted to the EMBL Data Library, February 1995
 A:Description: The sequence of S. cerevisiae cosmid 9672.
 A:Reference number: S59386

A/Accession: S59400
A/Molecule type: DNA
A/Residues: 1-1502 <JNH>
A/Cross-references: EMBL:U20865; NID:g662330; PIND:AA67387.1; PID:g662331; GSPDB:GN0001
A/Experimental source: strain 5288C (AB972)
R/RefSeq: K.; Kim, K.S.; Kogan, S.; Guarente, L.
Cell 56, 291-301, 1989
A/Title: Functional dissection and sequence of yeast HAP1 activator.
A/Reference number: A13112; MUID:89106221; PMID:2643482
A/Accession: A13112
A/Molecule type: DNA
A/Residues: 1-144, 'I', 146-322, 'R', 324-454, 'N', 456-507, 'M', 509-586, 'K', 588-882, 'N', 884-95
A/Cross-references: EMBL:J03152; NID:g171645; PIND:AAA34662.1; PID:g171646
R/Cruisot, F.; Verdier, J.; Galsene, M.; Slonimski, P.P.
J. Mol. Biol. 204, 263-276, 1988
A/Title: CYP1 (HAP1) regulator of oxygen-dependent gene expression in yeast. I. Overall
A/Reference number: S15447; MUID:89125585; PMID:2851658
A/Accession: S15447
A/Molecule type: DNA
A/Residues: 1-62, 'R', 64-1305, 'Y', 1306-1470, 'LVDFYADPFIWE' <CRE1>
A/Cross-references: EMBL:X13793
A/Note: The sequence is from mutant CYP1-18
C/Genetics: 8
A/Gene: SGD:HAP1; CYP1; MIPS:YLR256w
A/Cross-references: SGD:S0004246; MIPS:YLR256w
A/Map position: 12R
C/Superfamily: regulatory protein HAP1; GAL4 zinc binuclear cluster homology
C/Keywords: DNA binding; heme binding; transcription regulation; zinc finger
F:1-148/Domain: DNA binding #status predicted <DNA>
F:59-98/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F:64-84/Region: zinc finger CCCC motif
F:177-189/Region: glutamine-rich
F:245-445/Domain: heme binding #status predicted <HEM>
F:298-304, 323-328, 347-352, 373-378, 389-394, 415-420/Region: 6-residue repeats
F:1308-1481/Domain: activation element #status predicted <ACT>
F:1388-1481/Region: acidic
Query Match 11.8%; Score 78.5; DB 1; Length 1502;
Best Local Similarity 20.6%; Pred. No. 28;
Matches 35; Conservative 29; Mismatches 43; Indels 63; Gaps 7;
Qy 23 PRGVN-PTNGVASI-----SQGAVPALEKRVTVSVS 53
Db 1278 PRGISPKDSNGLSVQPLSPFSMNQNGRTIPVPSLITNITSQMGALPSLDRITNQIN 1337
Qy 54 QPSRR-KNYKQVQICNP-----TACTANGSCP 82
Db 1338 LPDPBRDAFDSISIKQMPMTSAFMANNTTIPSSITLNGNMNNGAGTANTDTTSANGSALS 1397
Qy 83 SVTRQAVADV-TFSEFYSTD-EERAFVTELLALASP-LTIDAIDQLN 129
Db 1398 TLTSQGSDDLANSNATQYKPDLEDFLMONSFNGLMNPSSLVEVGGIN 1447
RESULT 14
S57537
MKTI protein - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein N2302; protein YNL085w
C/Species: Saccharomyces cerevisiae
C/Date: 10-Oct-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S57537; S50279; S63024; S63017; S65096
R/Soler-Mira, A.; Saliz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A/Reference number: S57537
A/Accession: S57537
A/Molecule type: DNA
A/Residues: 1-830 <SOI>
A/Cross-references: UNIPROT:P40850; EMBL:X89016; NID:g887621; PID:g887626
R/Vermet, M.; Widner, W.R.; Dimman, J.D.; Wickner, R.B.
Yeast 10, 1477-1479, 1994
A/Title: Sequence of MKTI, needed for propagation of M(2) satellite dsRNA of the L-A virus
A/Reference number: S50279; MUID:95176705; PMID:7532890
A/Accession: S50279

A/Molecule type: DNA
A/Residues: 1-29, 'G', 31-808, 'TMKTCTNYH' <VER>
A/Cross-references: EMBL:U09129; NID:g520475; PIND:AA69470.1; PID:g520476
R/Soler-Mira, A.; Saliz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A/Reference number: S63018
A/Accession: S63024
A/Molecule type: DNA
A/Residues: 1-830 <SON>
A/Cross-references: EMBL:Z71361; NID:g1301982; PID:g1301983; MIPS:YNL085w
A/Experimental source: strain 5288C
R/Poehlmann, R.; Philippen, P.
submitted to the Protein Sequence Database, April 1996
A/Reference number: S62997
A/Accession: S63017
A/Molecule type: DNA
A/Residues: 569-830 <ROE>
A/Cross-references: EMBL:Z71361; MIPS:YNL085w
A/Experimental source: strain 5288C
R/Soler-Mira, A.; Saliz, J.E.; Ballesta, J.P.G.; Remacha, M.
Yeast 12, 485-491, 1996
A/Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
A/Reference number: S65092; MUID:96310628; PMID:8740422
A/Accession: S65096
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-830 <SOF>
A/Cross-references: EMBL:X89016; NID:g887621; PIND:CAA61425.1; PID:g887626
C/Genetics: 8
A/Gene: SGD:MKTI
A/Cross-references: SGD:S0005029; MIPS:YNL085w
A/Map position: 14L
C/Superfamily: Saccharomyces cerevisiae MKTI protein
C/Keywords: transmembrane protein
F:615-631/Domain: transmembrane #status predicted <TM>

Query Match 11.8%; Score 78; DB 2; Length 830;
Best Local Similarity 24.8%; Pred. No. 16;
Matches 25; Conservative 23; Mismatches 47; Indels 6; Gaps 3;
Qy 5 TTTGNTGKQKQITLVNPRGVNPTNGVASISQAGVPALEKRVTVSVSOPSRRKNKYV 64
Db 301 STTLQN--DSKENTQNYQGISALRYMPVLDKGVKLPFOEIVSSEDSKNNKDGK- 356
Qy 65 QVKIONPTACTANGSCDPSVTROAVADYVTFSTQSTDEER 105
Db 357 KSNLSSPSSASSASAPATTVTKNSKLYE--KSTIKYVR 395

RESULT 15
C98221
hypothetical protein AGR_L1428 (imported) - Agrobacterium tumefaciens (strain C58, Cerec
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: C98221
R/Goodner, B.; Hinkle, G.; Galtung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: C98221
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-136 <KUR>
A/Cross-references: UNIPROT:O808F3; GB:AB007870; PIND:AAK89293.1; PID:g15159127; GSPDB:GN
A/Gene: AGR_L1428
A/Map position: linear chromosome
Query Match 11.7%; Score 77.5; DB 2; Length 136;
Best Local Similarity 25.4%; Pred. No. 2.2;
Matches 30; Conservative 14; Mismatches 57; Indels 17; Gaps 3;

QY 11 ICKDKQKQTLVLPNGVNPNGVAVSQAQAV-----PALEKRVTVSVSQPSRNR 59
| | | | | : | | : | : | :
Db 3 ISKDKQKQTESADPHWIEWVTGTITLLVAMFGWIAVDIYRYSPEARFEIAVTGVEGQT 62
QY 60 KNYKVQVKIQNPACTA-----NGSCDPSVTRQAYADVTFSF-TQYSTDEBRAPVTE 111
| | : | | : | | : | | : | : | :
Db 63 GQYRVKFAIHNLSTTAQVNVRGDLEQNGASPENADVTFDYVASESKDNGTLFPRSD 120

Search completed: January 4, 2005, 09:17:26
Job time : 9.03224 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663
Sequence: 1 AKETVTYGNIGKDKQRTIV.....AALLASPLLIDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	132	1	COAT_BPOBE
2	663	100.0	133	1	AAAM3126
3	663	100.0	329	2	Q8L7E1
4	663	100.0	329	2	AAAI6663
5	572	86.3	133	2	Q9T0R9
6	572	86.3	329	2	Q9T0R9
7	552	83.3	133	2	Q9T0S0
8	552	83.3	329	2	Q9T0S0
9	537.5	81.1	132	1	COAT_BPSP
10	537.5	81.1	331	1	VAL_BPSP
11	501.5	75.6	132	2	Q9T0R8
12	501.5	75.6	330	2	Q64310
13	117	17.6	131	1	COAT_BPFR
14	95.5	14.4	473	1	Q8VDC2
15	94.5	14.3	530	1	TACY_LISSE
16	94.5	14.3	530	2	AAAR97361
17	93.5	14.1	540	2	Q48683
18	89.5	13.5	529	1	TACY_LISMF
19	89.5	13.5	529	1	TACY_LISMO
20	89.5	13.5	529	2	Q9L5B9
21	89.5	13.5	529	2	Q6E9A2
22	89.5	13.5	529	2	Q6E9A2
23	89.5	13.5	529	2	Q6E9A2
24	89.5	13.5	529	2	Q6E9A2
25	89.5	13.5	529	2	Q6E9A2
26	89.5	13.5	529	2	Q6E9A2
27	89.5	13.5	529	2	Q6E9A2
28	89.5	13.5	529	2	Q6E9A2
29	89.5	13.5	529	2	Q6E9A2
30	89.5	13.5	529	2	Q6E9A2
31	89.5	13.5	529	2	AAAT03000

32	81	12.2	129	1	COAT_BPUP3	P34700 bacterioph
33	80	12.1	129	1	COAT_BPQA	P07234 bacterioph
34	80	12.1	130	2	Q9WBL2	Q9WBL2 bacterioph
35	80	12.1	336	2	Q8TRF3	Q8TRF3 methanosa
36	80	12.1	1624	2	Q9V3K8	Q9V3K8 dirosophi
37	80	12.1	1637	2	Q9SRU8	Q9SRU8 dirosophi
38	79	11.9	432	2	P91584	P91584 cioma inte
39	79	11.9	461	2	Q7PP73	Q7PP73 anopheles
40	78.5	11.8	528	1	TACY_LISIV	P31831 listeria iv
41	78.5	11.8	528	2	Q6R6D9	Q6R6D9 listeria iv
42	78.5	11.8	528	2	AAAR97343	AAAR97343 listeria
43	78.5	11.8	608	2	Q84H79	Q84H79 rhodococcus
44	78.5	11.8	1502	1	CYPL_YEAST	P12351 saccharomyc
45	78	11.8	830	1	MKT1_YEAST	P40850 saccharomyc

ALIGNMENTS

RESULT 1
ID COAT_BPOBE STANDARD; PRT; 132 AA.
AC P0615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alloviridae;
OK NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielens I., Dreilima D., Dislers A., Baumanis V.,
Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarots C., Sastre P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
bacteriophage Q-beta as an application of a mapping procedure for RNA
fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=7118576; PubMed=838709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maiz T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bundule M., Valgaard K., Liljae L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
-1- FUNCTION: Forms the phage shell; binds to the phage RNA.

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CC EMBL; M99039; AAA16662.1; -
 CC EMBL; V00643; CAA23992.1; -
 DR PIR; A92240; VCBPOB.
 DR PDB; 1QBE; X-ray; A/B/C=1-132.
 DR InterPro; IPR002703; Lev1_coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
 FT INIT MET 0 0
 FT CONFLICT 22 22 N -> D (in Ref. 4).
 FT CONFLICT 56 56 Missing (in Ref. 4).
 FT STRAND 6 9
 FT TURN 13 14
 FT STRAND 18 27
 FT TURN 28 31
 FT STRAND 32 36
 FT HELIX 42 44
 FT STRAND 47 53
 FT STRAND 56 56
 FT TURN 57 58
 FT STRAND 59 59
 FT STRAND 62 74
 FT STRAND 83 96
 FT TURN 98 99
 FT HELIX 102 117
 FT HELIX 119 126
 FT TURN 127 127
 SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA572E CRC64;

Query Match 100.0%; Score 663; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2,2e-56;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVASTSQAGAVPALERKRVTVSVSQPSRRNK 60
 DB 1 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVASTSQAGAVPALERKRVTVSVSQPSRRNK 60
 QY 61 NRVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEERAFVTELAALLASPL 120
 DB 61 NRVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEERAFVTELAALLASPL 120
 QY 121 LIDALDQNPAY 132
 DB 121 LIDALDQNPAY 132

RESULT 2
 AAM33126. PRELIMINARY; PRT; 133 AA.
 ID AAM33126;
 AC AAM33126;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Coat protein.
 OS Bacteriophage Q-beta.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviridae; Alloviridae subgroup III.
 OC NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Bacher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes."
 RL BMC Evol. Biol. 3:24-24(2003).
 DR EMBL; AY09114; AAM33126.1; -.
 KM Coat protein.
 SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 100.0%; Score 663; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 2,2e-56;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVASTSQAGAVPALERKRVTVSVSQPSRRNK 60
 DB 2 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVASTSQAGAVPALERKRVTVSVSQPSRRNK 61
 QY 61 NRVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEERAFVTELAALLASPL 120
 DB 62 NRVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEERAFVTELAALLASPL 121
 QY 121 LIDALDQNPAY 132
 DB 122 LIDALDQNPAY 133

RESULT 3
 Q8LTEL1 PRELIMINARY; PRT; 329 AA.
 ID Q8LTEL1;
 AC Q8LTEL1;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE A1 read-through protein (A1 protein).
 OS Bacteriophage Q-beta.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Alloviridae;
 OC NCBI_TaxID=12009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14667253;
 RA Bacher J.M., Bull J.J., Ellington A.D.;
 RT "Evolution of phage with chemically ambiguous proteomes."
 RL BMC Evol. Biol. 3:24-24(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94109687; PubMed=7506687;
 RA Kozlovskaya T.M., Chelens I., Dreilima D., Dislers A., Baumanns V.,
 RA Ose V., Pumpens P.;
 RT "Recombinant RNA phage Q beta capsid particles synthesized and self-assembled in Escherichia coli."
 RL Gene 137:133-137(1993).
 DR EMBL; AY09114; AAM33127.1; -.
 DR EMBL; M99039; AAA16663.1; -.
 DR HSP; P03615; 1QBE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; P:Structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1_coat.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR PROSITE; PS00030; RNP_RNP_1; UNKNOWN 1.
 DR PROSITE; PS00030; RNP_RNP_1; UNKNOWN 1.
 SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 100.0%; Score 663; DB 2; Length 329;
 Best Local Similarity 100.0%; Pred. No. 6,4e-56;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVASTSQAGAVPALERKRVTVSVSQPSRRNK 60
 DB 2 AKLETVTLGNIGKDGKQTLVLPNGVNPNGVASTSQAGAVPALERKRVTVSVSQPSRRNK 61
 QY 61 NRVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEERAFVTELAALLASPL 120
 DB 62 NRVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEERAFVTELAALLASPL 121
 QY 121 LIDALDQNPAY 132
 DB 122 LIDALDQNPAY 133

RESULT 4
 AAA16663 PRELIMINARY; PRT; 329 AA.
 ID AAA16663;
 AC AAA16663;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)


```
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DS A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allicolevirus.
OX NCBI_TaxID=12009;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Clelens I., Dreilima D., Dielers A., Baumanis V.,
RA Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
RT assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL, M99039; AAA1663.1; -
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 100.0%; Score 663; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 6,4e-56;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEETVLTGNIKDKQKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRNK 60
DB 2 ALEETVLTGNIKDKQKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
AC Q9TOR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allicolevirus.
OX NCBI_TaxID=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder M.J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBD databases.
DB EMBL, AF059242; AAC14699.1; -.
DR HSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; R:structural molecule activity; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 86.3%; Score 572; DB 2; Length 329;
Best Local Similarity 84.1%; Pred. No. 4,4e-47;
Matches 111; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
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Query Match 86.3%; Score 572; DB 2; Length 133;
Best Local Similarity 84.1%; Pred. No. 1,5e-47;
Matches 111; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 ALEETVLTGNIKDKQKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRNK 60
DB 2 ALEETVLTGNIKDKQKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIQNPCTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPCTANGSCDPSVTRQAVADVTFFSTQYSTDEERAFVTELAALLADPM 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allicolevirus.
OX NCBI_TaxID=75723;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder M.J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN (3)
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBD databases.
DB EMBL, AF059242; AAC14700.1; -.
DR HSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; R:structural molecule activity; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 86.3%; Score 572; DB 2; Length 329;
Best Local Similarity 84.1%; Pred. No. 4,4e-47;
Matches 111; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
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RESULT 7
Q9T0S0 PRELIMINARY; PRT; 133 AA.
ID Q9T0S0;
AC Q9T0S0;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Coat protein. M11.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A11olevivirus.
OX NCBI_Taxid=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KW Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 098722336C3A255 CRC64;

Query Match 83.3%; Score 552; DB 2; Length 133;
Best Local Similarity 81.1%; Pred. No. 1.3e-45;
Matches 107; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 AKLETVTIGNIGKDGKQTLVLPNGVNPPTNGVVASLSQAGVPALEKRVTVSVSOPSRNK 60
DB 2 AKLQATITLSGIGKKDVTLDLPNGVNPPTNGVVALEAGVPALEKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALASPL 120
DB 62 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALADPM 121
QY 121 LIDAIQDLPAY 132
DB 122 LVNAIDNLPAY 133

RESULT 8
O64303 PRELIMINARY; PRT; 329 AA.
ID O64303;
AC O64303;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE A1-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A11olevivirus.
OX NCBI_Taxid=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06251.1; -.
DR HSSP; P03615; IQBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Levi_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35893 MW; 3B33CDB21E625F4 CRC64;

Query Match 83.3%; Score 552; DB 2; Length 329;
Best Local Similarity 81.1%; Pred. No. 3.8e-45;
Matches 107; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 AKLETVTIGNIGKDGKQTLVLPNGVNPPTNGVVASLSQAGVPALEKRVTVSVSOPSRNK 60
DB 2 AKLQATITLSGIGKKDVTLDLPNGVNPPTNGVVALEAGVPALEKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALASPL 120
DB 62 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEERAFVTELAALADPM 121
QY 121 LIDAIQDLPAY 132
DB 122 LVNAIDNLPAY 133

RESULT 9
COAT_BSP STANDARD; PRT; 132 AA.
ID COAT_BSP
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC A11olevivirus.
OX NCBI_Taxid=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07489; CAA0374.1; -.
DR HSSP; P03615; IQBE.

```

DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KW Coat protein; RNA-binding.
SQ SEQUENCE 132 AA; 14129 MW; 50B16CC6AFA0A254 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 132;
Best Local Similarity 79.5%; Pred. No. 3.4e-44;
Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQSPSRNK 60
DB 2 AKLNGVTLISKIGKNGDQTLTPRGVNPPTNGVASLSEAGAVPALERKVTVSQSPSRNK 61
QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NFKVQIKIQNPACTCRD-ACDPSVTRSAFADYTLSTSTDEERALLRTELAALLADPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IVDADININPAY 132

RESULT 10

VAL_BPSP STANDARD; PRT; 331 AA.
AC P06677;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Readthrough protein A1 (Contains: Coat protein).
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
NCBI_TaxId=12027;
RN NCBI_TaxId=12027;
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirschma A., Hirose T., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
protein sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X07489; CAB37299.1; -.
DR PIR; S01964; S01964.
DR HSSP; P03615; 10BE.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KW Coat protein.
FT CHAIN 1 132 Coat protein.
FT CHAIN 1 331 Readthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A6642B4B52C6582 CRC64;

Query Match 81.1%; Score 537.5; DB 1; Length 331;

Best Local Similarity 79.5%; Pred. No. 9.8e-44;
Matches 105; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQSPSRNK 60
DB 2 AKLNGVTLISKIGKNGDQTLTPRGVNPPTNGVASLSEAGAVPALERKVTVSQSPSRNK 61
QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
DB 121 IVDADININPAY 132

DB 62 NFKVQIKIQNPACTCRD-ACDPSVTRSAFADYTLSTSTDEERALLRTELAALLADPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IVDADININPAY 132

RESULT 11

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQSPSRNK 60
DB 2 AKLNGVTLISKIGKNGDQTLTPRGVNPPTNGVASLSEAGAVPALERKVTVSQSPSRNK 61
QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NFKVQIKIQNPACTCRD-ACDPSVTRSRDVTLSFTSTDEERALLRTELAALLADPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IVDADININPAY 132

Query Match 75.6%; Score 501.5; DB 2; Length 132;

Best Local Similarity 75.8%; Pred. No. 1e-40; Indels 1; Gaps 1;

Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQSPSRNK 60
DB 2 AKLNGVTLISKIGKNGDQTLTPRGVNPPTNGVASLSEAGAVPALERKVTVSQSPSRNK 61
QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NFKVQIKIQNPACTCRD-ACDPSVTRSRDVTLSFTSTDEERALLRTELAALLADPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IVDADININPAY 132

RESULT 12

QY 1 AKLEVTITGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKVTVSQSPSRNK 60
DB 2 AKLNGVTLISKIGKNGDQTLTPRGVNPPTNGVASLSEAGAVPALERKVTVSQSPSRNK 61
QY 61 NYKVQVLIQNPACTANGSCDPSVTRQAVADYTFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NFKVQIKIQNPACTCRD-ACDPSVTRSRDVTLSFTSTDEERALLRTELAALLADPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IVDADININPAY 132

OC Allotvivirus.
 OX NCBI_TaxID=75725;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95239761; PubMed=7723040;
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RT "Secondary structure model for the last two domains of single-stranded
 RNA phage Q beta.";
 RL J. Mol. Biol. 247:903-917 (1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190948; PubMed=8609616;
 RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
 RT "Secondary structure model for the first three domains of Q beta RNA.
 Control of A-protein synthesis.";
 RL J. Mol. Biol. 256:8-19 (1996).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF059243; AAC14704.1; -.
 DR HSSP; P03615; IQBE.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002703; Lev1 coat.
 DR InterPro; IPR000504; RNA_Tec_mot.
 DR Pfam; PF01819; Lev1_coat; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOMN.1.
 SQ SEQUENCE 330 AA; 36175 MW; 961855F408334410 CRC64;
 Query Match 75.6%; Score 501.5; DB 2; Length 330;
 Best Local Similarity 75.8%; Pred. No. 3e-40;
 Matches 100; Conservative 10; Mismatches 21; Indels 1; Gaps 1;
 QY 1 AKLETVTLGNIGKDGKQTLVLRGVNPTNGVSLGQAGVPLERKVTYSVSQPSRNK 60
 DB 2 AKLNKVLTLTGIGKAGNLTILTRGVNPTNGVSLSEAGVPLERKVTYSVAQPSRNK 61
 QY 61 NYKVQVNIQNPCTANGSCDPSVTRQAVADVTFPSFYQSTDEERAVRTETLALIASPL 120
 DB 62 NYKVQVNIQNPCTANGSCDPSVTRQAVADVTFPSFYQSTDEERAVRTETLALIASPL 120
 QY 121 LIDALDQINPAY 132
 DB 121 IVDALDQINPAY 132
 RESULT 13
 COAT_BPPRR STANDARD; PRT; 131 AA.
 ID COAT_BPPRR
 AC P03616;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Coat protein.
 OS Bacteriophage PRL1.
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 CC unclassified leviviridae.
 OX NCBI_TaxID=12024;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=79148387; PubMed=107028;
 RA Dhasee P., Vandekerckhove J., van Montagu M.;
 RT "The primary structure of the coat protein of the broad-host-range RNA
 bacteriophage PRL1.";
 RL Eur. J. Biochem. 94:375-386 (1979).
 CC -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
 DR PIR; A04225; VCBPPI.
 DR InterPro; IPR002703; Lev1 coat.
 DR Pfam; PF01819; Lev1_coat; 1.
 KM Coat protein; direct protein sequencing; RNA-binding.
 SQ SEQUENCE 131 AA; 14535 MW; E7B639E1B50FC612 CRC64;

Query Match 17.6%; Score 117; DB 1; Length 131;
 Best Local Similarity 32.3%; Pred. No. 0.0021;
 Matches 42; Conservative 15; Mismatches 57; Indels 16; Gaps 5;
 QY 17 QTLVLRGVNPT-----NGVASLSQAGVPLERKVTYSVSQPSRNKRYKVQV 66
 DB 4 QNLVLKQREATPNDHTFVPDIRNVEVSGVPIGSRFTISLAKTNGR--YKSTL 61
 QY 67 KIQNP--ACTANGSCDPSVTRQAVADVTFPSFYQSTDEER-AVETELALIASPLII- 122
 DB 62 KLVVPVQSVQVNIQNPCTANGSCDPSVTRQAVADVTFPSFYQSTDEERAVRTETLALIASPL 121
 QY 123 DAIDQINPAY 132
 DB 122 DTIVNLQGVY 131
 RESULT 14
 Q8VDC2 PRELIMINARY; PRT; 473 AA.
 ID Q8VDC2
 AC Q8VDC2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transmembrane protein 7.
 GN Name=Trmem7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=22350095; PubMed=12461651;
 RA Kiss H., Darai E., Kiss C., Kost-Allmova M., Klein G., Dumanaki J.P.,
 RA Imreh S.;
 RT "Comparative human/murine sequence analysis of the common eliminated
 region 1 from human 3p21.3.";
 RL Mamm. Genome 13:646-655 (2002).
 DR EMBL; AJ428064; CAD20986.1; -.
 DR MGD; MGI:2446841; Trmem7.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 KM Transmembrane.
 SQ SEQUENCE 473 AA; 51994 MW; B1872E0E569F2A4D CRC64;
 Query Match 14.4%; Score 95.5; DB 2; Length 473;
 Best Local Similarity 25.4%; Pred. No. 1.2;
 Matches 45; Conservative 17; Mismatches 46; Indels 69; Gaps 7;
 QY 5 TTTLGNIGKDGKQTLV-----LNRGVNPTNG--VASLSQAGVPLERKVTYSVSQPSRNK 46
 DB 195 TATCSNIISSOPSSKQVQKQASKANPQASNPYKNDPKVCSKPPAPPLSPISLSKAREP 254
 QY 47 RVTVASVQPSRNKRYKVQV-----KIQNP-----ACTANGSCDPSVTRQAV--- 89
 DB 255 KATVTSNIISSRSSSKQVQKQASKANPQASNPYKNDPKVCSKPPAPPLSPISLSKAREP 314
 QY 90 -----ADVTFPSFYQSTDEERAVRTETLALIASPLII 122
 DB 315 SPAPAPCTVIQWPSPTPIDGSRADVAKENRSTRKPK-----ALLSSPLYV 361
 RESULT 15
 TACY_LISSE STANDARD; PRT; 530 AA.
 ID TACY_LISSE
 AC P31830;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Seeligeryolysin precursor (thiol-activated cytolysin).
 GN Name=Isc;
 OS Listeria seeligeri.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

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OM protein - protein search, using SW model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663
Sequence: 1 AKLEVTYIGNIGKQKQTLV.....ALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23sep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	132	5	ABG94233 Bacterioph
2	663	100.0	132	5	ABG80545 Bacterioph
3	663	100.0	132	6	ABR56439 Bacterioph
4	663	100.0	132	6	ABU09686 Bacterioph
5	663	100.0	132	6	ABR44542 Bacterioph
6	663	100.0	132	7	ADD24117 Bacterioph
7	663	100.0	132	7	ADJ82043 Protein f
8	663	100.0	132	7	ADK17131 Virus-11k
9	663	100.0	132	8	ADJ36300 Bacterioph
10	663	100.0	132	8	ADJ67146 Bacterioph
11	663	100.0	132	8	ADK52180 Bacterioph
12	663	100.0	328	6	ABR56440 Bacterioph
13	663	100.0	328	6	ABR44543 Bacterioph
14	663	100.0	329	5	ABG94278 Bacterioph
15	663	100.0	329	5	ABG80590 Bacterioph
16	663	100.0	329	6	ABU09687 Bacterioph
17	663	100.0	329	7	ADD24118 Bacterioph
18	663	100.0	329	7	ADJ82044 Protein f
19	663	100.0	329	7	ADK17132 Virus-11k
20	663	100.0	329	8	ADJ36301 Bacterioph
21	663	100.0	329	8	ADJ67147 Bacterioph
22	663	100.0	329	8	ADK52181 Bacterioph
23	655	98.8	132	5	ABG94316 Bacterioph
24	655	98.8	132	5	ABG94330 Bacterioph
25	655	98.8	132	5	ABG80632 Bacterioph

26	655	98.8	132	5	ABG80628 Bacterioph
27	655	98.8	132	6	ABR56455 Bacterioph
28	655	98.8	132	6	ABR56452 Bacterioph
29	655	98.8	132	6	ABU09689 Bacterioph
30	655	98.8	132	6	ABU09693 Bacterioph
31	655	98.8	132	6	ABR44555 Bacterioph
32	655	98.8	132	6	ABR44558 Bacterioph
33	655	98.8	132	7	ADD24130 Bacterioph
34	655	98.8	132	7	ADD24133 Bacterioph
35	655	98.8	132	7	ADJ82059 Protein f
36	655	98.8	132	7	ADJ82056 Protein f
37	655	98.8	132	7	ADK17144 Virus-11k
38	655	98.8	132	7	ADK17147 Virus-11k
39	655	98.8	132	8	ADJ36316 Bacterioph
40	655	98.8	132	8	ADJ36313 Bacterioph
41	655	98.8	132	8	ADJ67159 Phase Ope
42	655	98.8	132	8	ADJ67162 Phase Ope
43	655	98.8	132	8	ADK52196 Bacterioph
44	655	98.8	132	8	ADK52193 Bacterioph
45	652	98.3	132	5	ABG94318 Bacterioph

ALIGNMENTS

RESULT 1	ABG94233	standard; protein; 132 AA.
ID	ABG94233	
XX	ABG94233;	
XX	06-AUG-2003 (revised)	
DT	10-DEC-2002 (first entry)	
XX	Bacteriophage coat protein #1.	
DE	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;	
KW	cytotoxic; antiviral; antidiabetic; hypoglycaemic; antigen array;	
KW	vaccine; infectious disease.	
XX	Bacteriophage.	
OS	WO200256905-A2.	
PN	25-JUL-2002.	
XX	21-JAN-2002; 2002WO-1B000166.	
PF	19-JAN-2001; 2001US-0262379P.	
XX	04-MAY-2001; 2001US-0288549P.	
PR	05-OCT-2001; 2001US-0326988P.	
PR	07-NOV-2001; 2001US-0331045P.	
XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
PA	Renner WA, Bachmann M, Tiesse A, Maurer P, Lechner F, Sebbel P;	
PI	Ploesek C;	
PI	WPI, 2002-627351/67.	
XX	Molecular antigen array used in the production of vaccines for infectious	
XX	diseases.	
PS	Claim 13; Page 379; 441pp; English.	
XX	This invention relates to a novel ordered and repetitive antigen array	
CC	used in the production of vaccines for infectious diseases. The invention	
CC	also discloses a composition comprising a non-natural molecular scaffold	
CC	comprising a core particle selected from a core particle of a non-natural	
CC	origin and a core particle of natural origin and an organiser comprising	
CC	at least one first attachment site, where the organiser is connected to	
CC	the core particle by at least one covalent bond. Also disclosed is an	
CC	antigen or antigenic determinant with at least one second attachment	

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Obeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 06
 CC -Aug-2003 to correct OS field.)

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 9.6e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYTGNIKGDKQKTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 60
 DB 1 AKLEVTYTGNIKGDKQKTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 60
 QY 61 NKQVQVKIQNPACTGANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFVTELAALLASPL 120
 DB 61 NKQVQVKIQNPACTGANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 2
 ABG80545
 ID ABG80545 standard; protein; 132 AA.

XX ABG80545;
 AC
 XX 29-AUG-2003 (revised)
 DT 29-NOV-2002 (first entry)
 XX

DE Bacteriophage Q-beta coat protein.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.

XX Bacteriophage Qbeta.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-1B000168.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326998P.

XX 07-NOV-2001; 2001US-0331045P.

XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEO) LUEOEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 PI Maurer P., Lechner F., Ortmann R., Lueoend R., Staufenbiel M., Frey P;
 PI Renner WA, Bachmann M, Tissot A, Seibel P, Piossek C;
 XX WPI; 2002-636514/68.

PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.

PS Disclosure; Page 356-357; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array. (Updated on 29-AUG-
 CC 2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 9.6e-70;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTYTGNIKGDKQKTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 60
 DB 1 AKLEVTYTGNIKGDKQKTLVLPNGVPTNGVASISQAGAVPALEKRVTVSVSOPSRRNK 60
 QY 61 NKQVQVKIQNPACTGANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFVTELAALLASPL 120
 DB 61 NKQVQVKIQNPACTGANGSCDPSVTRQAVADVTFSFTQYSTDEBRAFVTELAALLASPL 120
 QY 121 LIDAIDQINPAY 132
 DB 121 LIDAIDQINPAY 132

RESULT 3
 ABR56439

ABR56439 standard; protein; 132 AA.
AC ABR56439;
DT 23-OCT-2003 (revised)
DT 28-JUL-2003 (first entry)
DE Bacteriophage Q-beta coat protein SEQ ID NO:10.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
XX cytosolic; virucide; antibacterial; antiparasitic; fungicide;
XX antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
XX antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
XX antineumatic; antiarthritic; vaccine; immunisation; infectious disease;
XX anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
XX graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
XX Alzheimer's disease; osteoporosis; rheumatoid arthritis;
XX inflammatory autoimmune disease.
XX Bacteriophage Qbeta.
OS WO2003024480-A2.
PN 27-MAR-2003.
XX
XX 16-SEP-2002; 2002WO-IB004252.
XX 14-SEP-2001; 2001US-0318967P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX Bachmann M, Stornl T, Lechner F,
XX WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
XX or a virus-like particle, enhancing anti-viral protection in an animal,
XX PT or immunising or treating tumors or infectious diseases, e.g. viral
XX infections.
XX
XX Disclosure; Page 167-168; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
XX response against an antigen or a virus-like particle in an animal. (C)
XX comprises a virus-like particle (VLP) bound to at least one antigen, or a
XX VLP capable of being recognised by the immune system of the animal. Also
XX described: (1) enhancing an immune response against an antigen or a VLP
XX in an animal comprising introducing (C) into the animal; (2) vaccines
XX comprising (C) together with a pharmaceutical diluent, carrier or
XX excipient; (3) immunising or treating an animal comprising administering
XX the vaccine to the animal, or priming or boosting a T cell response in
XX the animal by administering the vaccine; and (4) enhancing anti-viral
XX protection in an animal comprising introducing (C) into the animal. (C)
XX has cytosolic, virucide, antibacterial, antiparasitic, fungicide,
XX antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
XX antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
XX antineumatic and antiarthritic activities. (C) or the vaccines can be
XX used for enhancing an immune response against an antigen or a VLP in an
XX animal, enhancing anti-viral protection in an animal, or immunising or
XX treating tumors and infectious diseases such as viral, bacterial,
XX parasitic or fungal infections. The vaccine compositions are also useful
XX for preventing or treating allergies, drug addiction, graft-versus-host
XX disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
XX Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
XX autoimmune disease. ACC65988 to ACC65982 and ABR56401 to ABR56599
XX represent sequences used in the exemplification of the present invention.
XX (Updated on 23-OCT-2003 to standardise OS field)
XX
XX Sequence 132 AA;
SQ
Query Match 100.0%; Score 663; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVTIGNIGKDKQTLVLPNGVPTNGVASLSQAGAVPALKKRYTVSVSOPSRRNK 60
DB 1 AKLETVTIGNIGKDKQTLVLPNGVPTNGVASLSQAGAVPALKKRYTVSVSOPSRRNK 60
QY 61 NKVGVKIQNPACTANGSCDPSVTRQAVADTVSFSTQSTEEBAFVTELAALLASPL 120
DB 61 NKVGVKIQNPACTANGSCDPSVTRQAVADTVSFSTQSTEEBAFVTELAALLASPL 120
QY 121 LIDAIDQNPAY 132
DB 121 LIDAIDQNPAY 132
RESULT 4
ID ABR09686 standard; protein; 132 AA.
XX ABR09686;
AC ABR09686;
XX
XX 03-JUL-2003 (first entry)
XX
XX Bacteriophage Qbeta coat protein CP.
DE Bacteriophage Qbeta; coat protein; CP; hypotensive; cerebroprotective;
XX Bacteriophage Qbeta; coat protein; CP; hypotensive; cerebroprotective;
XX cardiast; nephroprotective; ophthalmological; immunostimulant; vaccine;
XX angiotensin peptide moiety carrier conjugate; angiotensin peptide;
XX renin-activated angiotensin system; hypertension; stroke; infarction;
XX congestive heart failure; kidney failure; retinal haemorrhage.
XX
XX Bacteriophage Qbeta.
XX
XX WO2003031466-A2.
XX
XX 17-APR-2003.
XX
XX 07-OCT-2002; 2002WO-EP011219.
XX
XX 05-OCT-2001; 2001US-0326998P.
XX 07-NOV-2001; 2001US-0331045P.
XX 18-JAN-2002; 2002US-00050902.
XX 21-JAN-2002; 2002WO-IB000166.
XX 19-JUL-2002; 2002US-0396637P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M;
XX
XX WPI; 2003-430264/40.
XX
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
XX an angiotensin peptide moiety useful for treating or preventing a
XX disorder associated with renin-activated angiotensin, e.g. hypertension
XX or infarction.
XX
XX Claim 15; Page 92; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate
XX comprising: (a) a carrier with at least one first attachment site; and
XX (b) at least one angiotensin peptide moiety with at least one second
XX attachment site. The angiotensin peptide moiety and compositions
XX comprising them are useful for immunising an animal against an
XX angiotensin peptide, and for treating or preventing a physical disorder
XX associated with renin-activated angiotensin system such as hypertension,
XX stroke, infarction, congestive heart failure, kidney failure, and retinal
XX haemorrhage. The conjugate is also useful for inducing immune response,
XX including producing antibodies. This is the amino acid sequence of
XX bacteriophage Qbeta coat protein CP used in the preparation of the
XX vaccine conjugates of the invention
XX
XX Sequence 132 AA;
SQ
Query Match 100.0%; Score 663; DB 6; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.66-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTLTGNIGKDKQKQTLVNPBGVPTNGVASLSQAGAVPALBKRYTVSVSOPSRRNK 60
DB 1 AKLEVTLTGNIGKDKQKQTLVNPBGVPTNGVASLSQAGAVPALBKRYTVSVSOPSRRNK 60

QY 61 NYKVQVKIQNPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBFAFVTELLAALLASPL 120
DB 61 NYKVQVKIQNPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBFAFVTELLAALLASPL 120

QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 5
ABR44542
ID ABR44542 standard; protein; 132 AA.
XX
AC ABR44542;
XX
DT 23-OCT-2003 (revised)
DT 25-JUL-2003 (first entry)

Bacteriophage Q-beta coat protein SEQ ID NO:10.

XX
DE Bacteriophage Q-beta coat protein; HBV; LCMV;
XX immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
XX hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
XX immunostimulant; cytotoxic; antiallergic; viral disease; hepatitis;
XX immune response; immunization; allergy; tumor; breast cancer;
XX neuroblastoma; leukemia; viral disease; influenza; hepatitis; measles;
XX chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

OS Bacteriophage Qbeta.
XX
XX WO2003024481-A2.
XX
XX
XX 27-MAR-2003.
XX
XX
XX 16-SEP-2002; 2002WO-IB004132.
XX
XX 14-SEP-2001; 2001US-0318994P.
XX 22-APR-2002; 2002US-0374145P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX (MAURER) MAURER P.
XX (TISSOT) TISSOT A.
XX (SCHWAB) SCHWAB R.
XX (MEIJER) MEIJERINK E.
XX (LIPPO) LIPPOMSKY G.
XX (PUMP) PUMPENS P.
XX (CIETEL) CIETELNS I.
XX (RENNHOF) RENNHOF R.
XX
XX MAURER P., Tissot A., Schwarz K., Meijerink E., Lipowsky G.,
XX Pumpens P., Cielens I., Renhof R., Bachmann M., Storni T.,
XX
XX WPI; 2003-354564/33.
XX
XX New compositions comprising immunostimulatory substances packaged into
XX virus-like particles, useful as a vaccine for enhancing an immune
XX response in animals, e.g. for treating or preventing allergies, tumors or
XX viral infections.
XX
XX Disclosure; Page 247; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune
XX response in an animal. (C) comprises a virus-like particle (VLP), and an
XX immunostimulatory substance. The immunostimulatory substance is bound to
XX the VLP. Also described: (1) enhancing an immune response in an animal by
XX introducing (C) into the animal; (2) producing (C) for enhancing an
XX immune response in an animal; (3) vaccines comprising (C) together with a

CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
CC treating an animal by: (a) administering the vaccine to the animal; (b)
CC priming a T cell response in the animal by administering the vaccine; or
CC (c) boosting a T cell response in the animal by administering the
CC vaccine. (C) has immunostimulant, cytotoxic, antiallergic, virucide and
CC antibacterial activities. (1) can be used in vaccines for enhancing an
CC immune response in an animal, particularly a mammal or human.
CC Specifically, (C) is useful for enhancing a B cell response, a T cell
CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
CC comprising (C) can also be used for immunising or treating an animal,
CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
CC reptiles or fish. (C) is particularly useful in prophylactic or
CC therapeutic vaccines against allergies, tumors (e.g. breast cancers,
CC neuroblastoma, or leukemia), viral diseases (e.g. influenza, hepatitis,
CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
CC represent sequences used in the exemplification of the present invention.
CC (Updated on 23-OCT-2003 to standardise OS field)

XX SQ Sequence 132 AA;

Query Match 100.0%; Score 663; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.66-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTLTGNIGKDKQKQTLVNPBGVPTNGVASLSQAGAVPALBKRYTVSVSOPSRRNK 60
DB 1 AKLEVTLTGNIGKDKQKQTLVNPBGVPTNGVASLSQAGAVPALBKRYTVSVSOPSRRNK 60

QY 61 NYKVQVKIQNPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBFAFVTELLAALLASPL 120
DB 61 NYKVQVKIQNPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBFAFVTELLAALLASPL 120

QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 6
ADD24117
ID ADD24117 standard; protein; 132 AA.
XX
XX ADD24117;
XX
XX 15-JAN-2004 (first entry)
XX
XX
XX Bacteriophage Qbeta coat protein CP.
XX
XX
XX vaccine composition; virus-like particle; core particle;
XX first attachment site; antigen; antigenic determinant; prion protein;
XX PrP; PrP peptide; vaccine; neuroprotective; anti-inflammatory;
XX prion disease; Bovine Spongiform Encephalopathy; BSE;
XX Creutzfeldt-Jakob Disease; coat protein.
XX
XX
XX Bacteriophage Qbeta.
XX
XX WO2003059386-A2.
XX
XX
XX 24-JUL-2003.
XX
XX
XX 17-JAN-2003; 2003WO-BP000460.
XX
XX 18-JAN-2002; 2002US-00050902.
XX 21-JAN-2002; 2002WO-IB000166.
XX 08-JUL-2002; 2002US-0393725P.
XX 18-JUL-2002; 2002US-0396590P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M., Maurer P., Pelliccioli E., Renner WA,
XX
XX WPI; 2003-598483/56.
XX

PT A vaccine composition for preventing or treating prion diseases (e.g.
PT Creutzfeldt-Jakob Disease) comprising a virus-like particle (e.g. RNA-
PT phage) and at least one prion protein or peptide bound to the virus-like
PT particle.

PS Disclosure; SEQ ID NO 10; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
CC like or a core particle with at least one first attachment site and at
CC least one antigen or antigenic determinant that is a prion protein (PrP)
CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
CC being bound to the virus-like or core particle. The vaccine of the
CC invention may have neuroprotective or anti-inflammatory activity. The
CC composition is useful as a medicament or in manufacturing a medicament
CC for the treatment or prevention of prion diseases. The prion diseases may
CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
CC Disease. The present invention is the amino acid sequence of a coat
CC protein from a bacteriophage which may be used during the creation of the
CC vaccine composition of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKLEVTLTGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAPALKEKRVTVSVSOPSRNK 60

DB 1 AKLEVTLTGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAPALKEKRVTVSVSOPSRNK 60

OY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTEILAAALLASPL 120

DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTEILAAALLASPL 120

OY 121 LIDAIIDQINPAY 132

DB 121 LIDAIIDQINPAY 132

RESULT 7

ADJ82043 ID ADJ82043 standard; protein; 132 AA.

XX ADJ82043;

XX 06-MAY-2004 (first entry)

XX Protein for RANKL antigen array to treat bone disease.

XX osteopathic; vaccine; core particle; antigenic determinant; RANKL;

XX bone disease; encephalopathy; immune system stimulation.

XX Unidentified.

XX WO2003039225-A2.

XX 15-MAY-2003.

XX 07-NOV-2002; 2002WO-EP012449.

XX 07-NOV-2001; 2001US-0331045P.

XX 18-JAN-2002; 2002US-00050902.

XX 21-JAN-2002; 2002WO-1B000166.

XX 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Spohn G;

XX WPI; 2003-441430/41.

PT New compositions comprising a core particle and at least one antigen or
PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis

PT of bone diseases, particularly mammalian encephalopathies.

PS Disclosure; SEQ ID NO 10; 222pp; English.

XX The invention relates to a composition comprising a core particle having
CC at least one first attachment site, and at least one antigen or antigenic
CC determinant having at least one second attachment site. The antigen or
CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
CC peptide. The second attachment site is (non-) naturally occurring with
CC the antigen or antigenic determinant, and is capable of association with
CC the first attachment site. The antigen or antigenic determinant and the
CC core particle interact through the association to form an ordered and
CC repetitive antigen array. The composition is useful as a medicament, or
CC for the manufacture of a medicament for treating bone diseases. The
CC composition is especially useful for as a vaccine for therapy or
CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
CC and for stimulating mammalian immune system. This sequence represents a
CC protein of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKLEVTLTGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAPALKEKRVTVSVSOPSRNK 60

DB 1 AKLEVTLTGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAPALKEKRVTVSVSOPSRNK 60

OY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTEILAAALLASPL 120

DB 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTEILAAALLASPL 120

OY 121 LIDAIIDQINPAY 132

DB 121 LIDAIIDQINPAY 132

RESULT 8

ADK17131 ID ADK17131 standard; peptide; 132 AA.

XX ADK17131;

XX 06-MAY-2004 (first entry)

XX Virus-like particle repetitive antigen array peptide #10.

XX antiallergic; antiaesthetic; cytostatic; vaccine; virus-like particle;

XX interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;

XX allergic eosinophilic disease; asthma; Hodgkin's lymphoma.

XX Unidentified.

XX WO2003040164-A2.

XX 15-MAY-2003.

XX 07-NOV-2002; 2002WO-EP012455.

XX 07-NOV-2001; 2001US-0331045P.

XX 18-JAN-2002; 2002US-00050902.

XX 21-JAN-2002; 2002WO-1B000166.

XX 19-JUL-2002; 2002US-0396635P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Jennings G, Sonderegger I;

XX WPI; 2003-441518/41.

PT Composition comprising an ordered and repetitive antigen or antigenic
PT determinant array, useful as a medicament, or for manufacturing a

PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
 PT Hodgkin's lymphoma.

PS Disclosure; SEQ ID NO 10; 245bp; English.

XX The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC antigen with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medicaments, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 7; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.6e-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60

Db 1 AKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120

Db 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIDQLNPAY 132

Db 121 LIDAIDQLNPAY 132

RESULT 9
 ADJ36300 standard; protein; 132 AA.

AC ADJ36300;

DT 22-APR-2004 (first entry)

DE Bacteriophage Qbeta coat protein virus-like particle.

XX anti-allergic; cytostatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage Qbeta;
 KW coat protein; VLP; adjuvant.

OS Bacteriophage Qbeta.

XX WO2004000351-A1.

XX 31-DEC-2003.

PF 20-JUN-2003; 2003WO-EP006541.

PR 20-JUN-2002; 2002US-0389898P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann MF, Renner WA;

PS WPI; 2004-108361/11.

XX New compositions comprising a virus-like particle (VLP), an
 PT immunostimulatory substance bound to the VLP, and an antigen mixed with

PT the VLP, useful for enhancing immune response or for treating e.g. tumors
 PT or chronic viral diseases.

PS Example 5; SEQ ID NO 1; 252bp; English.

XX The invention describes a composition for enhancing an immune response in
 CC an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
 CC coat protein a virus like particle (VLP) that can be used in the adjuvant
 CC of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.6e-70;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60

Db 1 AKLEVTTLGNIGKDGKQTLVLPNGVPTNGVASLSQAGAVPALEKRYTVSVQPSRRK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120

Db 61 NYKVQVKIQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVTEIAALLASPL 120

QY 121 LIDAIDQLNPAY 132

Db 121 LIDAIDQLNPAY 132

RESULT 10
 ADJ67146 standard; protein; 132 AA.

ADJ67146;

DT 06-MAY-2004 (first entry)

DE Bacteriophage Qbeta coat protein for antigen display array.

XX anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
 KW antigenic array.

OS Bacteriophage Qbeta.

XX WO2004009124-A2.

XX 29-JAN-2004.

PF 18-JUL-2003; 2003WO-EP007849.

PR 19-JUL-2002; 2002US-0396638P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann MF, Fulurija A;

PS WPI; 2004-132866/13.

XX New composition comprising a core particle having a first attachment site
 PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
 PT peptide having a second attachment site, useful for treating obesity.

XX Claim 12; SEQ ID NO 4; 175bp; English.

XX The invention relates to a new composition comprising: (1) a core
 CC particle with at least one first attachment site; and (11) at least one
 CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
CC peptide, and where the second attachment site being consisting of an
CC attachment site not naturally occurring with the antigen or antigenic
CC determinant and an attachment site naturally occurring with the antigen
CC or antigenic determinant, where the second attachment site is capable of
CC association to the first attachment site, and where the ghrelin or a
CC ghrelin peptide and the core particle interact through the association to
CC form an ordered and repetitive antigen array. The composition is useful
CC for treating obesity. The repetitive array may form part of a phage or
CC bacterial display array. This peptide corresponds to a Bacteriophage
CC Qbeta coat protein which can used as part of the repetitive or antigenic
CC array.
XX
XX

SQ Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.66-70; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEBRAFYVTELAALLASPL 120
DB 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEBRAFYVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 11

ADK52180

ID ADK52180 standard; protein; 132 AA.

XX AC ADK52180;

XX DT 20-MAY-2004 (first entry)

XX DE Bacteriophage Qbeta coat protein CP.

XX KW neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;

XX KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;

XX KW coat protein; CP.

XX OS Bacteriophage Qbeta.

XX PN WO2004016282-A1.

XX PD 26-FEB-2004.

XX PF 18-JUL-2003; 2003WO-EP007864.

XX PR 19-JUL-2002; 2002US-0396639P.

XX PR 15-MAY-2003; 2003US-0470432P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PA (NOVS) NOVARTIS PHARMA AG.

XX PI Bachmann MF, Tisot A, Ortman R, Lueoend R, Straufenbiel M;

XX PI Frey P;

XX DR WPI; 2004-203731/19.

XX PT Composition comprising a core particle with at least one attachment site,

XX PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases

XX PT such as Alzheimer's disease.

XX PS Claim 12; SEQ ID NO 4; 184bp; English.

CC 1-6 peptide. The new composition comprises: a core particle with at least
CC one first attachment site; and at least one antigen or antigenic
CC determinant with at least one second attachment site, where the antigen
CC or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
CC second attachment site comprises: an attachment site not naturally
CC occurring with the antigen or antigenic determinant; or an attachment
CC site naturally occurring with the antigen or antigenic determinant. The
CC second attachment site is capable of association to the first attachment
CC site and the beta 1-6 peptide and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC composition is useful for the manufacture of a medicament for treating
CC Alzheimer's disease and related diseases. This is the amino acid sequence
CC of an RNA bacteriophage coat protein that can be used in the preparation
CC of the compositions and vaccines of the invention.
XX
XX

SQ Sequence 132 AA;

Query Match 100.0%; Score 663; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 9.66-70; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEBRAFYVTELAALLASPL 120
DB 61 NYKVQVKIOMPACTANGSCDPSVTRQAVADVTFSTQYSTDEBRAFYVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 12

ABR56440

ID ABR56440 standard; protein; 328 AA.

XX AC ABR56440;

XX DT 23-OCT-2003 (revised)

XX DT 28-JUL-2003 (first entry)

XX DE Bacteriophage Q-beta coat protein SEQ ID NO.11.

XX KW Antigen presenting cell; APC; immune response; virus like particle; VLP;

XX KW cytosolic; virucide; antibacterial; antiparasitic; fungicide;

XX KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;

XX KW antihypertoid; antidiabetic; neuroprotective; nootropic; osteopathic;

XX KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;

XX KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;

XX KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;

XX KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;

XX OS Bacteriophage Qbeta.

XX PN WO2003024480-A2.

XX PD 27-MAR-2003.

XX PF 16-SEP-2002; 2002WO-IB004252.

XX PR 14-SEP-2001; 2001US-0318967P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PA Bachmann MF, Storni T, Lechner F;

XX DR WPI; 2003-363095/34.

A composition, useful for enhancing an immune response against an antigen

or a virus-like particle, enhancing anti-viral protection in an animal,

PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX
PS Disclosure; Page 168-169; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumours and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 328 AA;
Query Match 100.0%; Score 663; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.6e-69;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVASTLSQAGAVPALERKVVVSQPSRNK 60
DB 2 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVASTLSQAGAVPALERKVVVSQPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTELAALIASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133
RESULT 13
ABR44543
ID ABR44543 standard; protein; 328 AA.
XX
AC ABR44543;
XX
DT 23-OCT-2003 (revised)
DT 25-JUL-2003 (first entry)
XX
XX Bacteriophage Q-beta coat protein SEQ ID NO:11.
XX
DE Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
XX hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
XX immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
XX immune response; immunisation; allergy; tumour; breast cancer;
XX neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
XX chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
OS Bacteriophage Qbeta.
XX
XX WO2003024481-A2.
XX
XX 27-MAR-2003.
PD

XX
XX 16-SEP-2002; 2002WO-IB004132.
PF
XX
XX 14-SEP-2001; 2001US-0318994P.
PR
XX 22-APR-2002; 2002US-0374145P.
PR
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (MAUR-) MAURER P.
PA (TISS-) TISSOT A.
PA (SCHW-) SCHWARZ K.
PA (MEIJ-) MEIJERINK E.
PA (LIPRO-) LIPOMSKY G.
PA (PUMP-) PUMPENS P.
PA (CIEL-) CIELENS I.
PA (RENH-) RENHOFA R.
XX
XX Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
PI Pumpens P, Cielens I, Renhofs R, Bachmann MP, Storni T;
PI
XX WPI; 2003-354564/33.
DR
XX
XX New compositions comprising immunostimulatory substances packaged into
PT virus-like particles, useful as a vaccine for enhancing an immune
PT response in animals, e.g. for treating or preventing allergies, tumors or
PT viral infections.
XX
XX Disclosure; Page 247-249; 322pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response in an animal. (C) comprises a virus-like particle (VLP), and an
CC immunostimulatory substance. The immunostimulatory substance is bound to
CC the VLP. Also described: (1) enhancing an immune response in an animal by
CC introducing (C) into the animal; (2) producing (C) for enhancing an
CC immune response in an animal; (3) vaccines comprising (C) together with a
CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
CC treating an animal by: (a) administering the vaccine to the animal; (b)
CC priming a T cell response in the animal by administering the vaccine; or
CC (c) boosting a T cell response in the animal by administering the
CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
CC antibacterial activities. (1) can be used in vaccines for enhancing an
CC immune response in an animal, particularly a mammal or human.
CC Specifically, (C) is useful for enhancing a B cell response, a T cell
CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
CC comprising (C) can also be used for immunising or treating an animal,
CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
CC reptiles or fish. (C) is particularly useful in prophylactic or
CC therapeutic vaccines against allergies, tumors (e.g. breast cancers,
CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
CC represent sequences used in the exemplification of the present invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 328 AA;
Query Match 100.0%; Score 663; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.6e-69;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVASTLSQAGAVPALERKVVVSQPSRNK 60
DB 2 AKLEVTTLNIGDKGQTLVLPNGVNPPTNGVASTLSQAGAVPALERKVVVSQPSRNK 61
QY 61 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTELAALIASPL 120
DB 62 NYKVQVKIONPTACTANGSCDPSVTRQAYADVTFSTQYSTDEBERAFVTELAALIASPL 121
QY 121 LIDAIDQINPAY 132
DB 122 LIDAIDQINPAY 133
RESULT 14

ABG94278
 ID ABG94278 standard; protein; 329 AA.
 AC ABG94278;
 XX
 XX
 DT 06-AUG-2003 (revised)
 DT 10-DEC-2002 (first entry)
 XX
 XX
 DE Bacteriophage Q beta coat protein A1.
 XX
 KM Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
 KM cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
 KM vaccine; infectious disease.
 XX
 OS Bacteriophage.
 XX
 WO200256905-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-1B000166.
 XX
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
 PI Piossek C;
 XX
 DR WPI: 2002-627351/67.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Claim 7; Page 416-417; 441pp; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Obeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 06
 CC -AUG-2003 to correct OS field.)
 XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 663; DB 5; Length 329;
 Best Local Similarity 100.0%; Pred. No. 3,66-69;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNK 60
 |||

DB 2 AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNK 61
 QY 61 NKVQVOKIOMPACTANGSCDPSVTRQAVADVFPSFTQSTDEERAFVTELAALLASPL 120
 DB 62 NKVQVOKIOMPACTANGSCDPSVTRQAVADVFPSFTQSTDEERAFVTELAALLASPL 121
 QY 121 LIDAIDQINPAY 132
 DB 122 LIDAIDQINPAY 133
 RESULT 15
 ABG80590
 ID ABG80590 standard; protein; 329 AA.
 XX
 AC ABG80590;
 XX
 DT 29-AUG-2003 (revised)
 DT 29-NOV-2002 (first entry)
 XX
 DE Bacteriophage Q-beta A1 protein.
 XX
 KM Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KM graft versus host disease; Igg-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enterokinase; cysteine-containing linker.
 XX
 OS Bacteriophage Qbeta.
 XX
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-1B000166.
 XX
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUDF/) LUDFEND R.
 PA (STAU/) STAUENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P, Lechner F, Ortmann R, Luedend R, Stauenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX
 DR WPI: 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Disclosure; Page 393-394; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is

CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and
CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The antigens are modified to possess
CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
CC virus like particle or bacterial protein (the scaffold protein). The
CC present sequence is bacterial protein or peptide which is coupled to the
CC modified antigen to form the molecular antigen array. (Updated on 29-AUG-
CC 2003 to standardise OS field)

XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 663; DB 5; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.6e-69;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AKLETTIGNIGKDGKOTLVNPRGVNPTNGVASTLSOAGAVPALBKRTVSVSQPSRNK	60
DB	2	AKLETVTLGNIGKDGKOTLVNPRGVNPTNGVASTLSOAGAVPALBKRTVSVSQPSRNK	61
QY	61	NYKVQKIQNPFTACTANGSCDPSVTRQAVADVTFSTQYSTDERAAFVTELAALLASPL	120
DB	62	NYKVQKIQNPFTACTANGSCDPSVTRQAVADVTFSTQYSTDERAAFVTELAALLASPL	121
QY	121	LIDAIQDLNPAY	132
DB	122	LIDAIQDLNPAY	133

Search completed: January 4, 2005, 09:10:58
Job time : 41.6824 secs

; TITLE OF INVENTION: Tuberculosis Vaccine

FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysomal
US-09-948-722-2

Query Match 13.5%; Score 89.5; DB 4; Length 626;
Best Local Similarity 23.5%; Pred. No. 0.027;
Matches 31; Conservative 23; Mismatches 43; Indels 35; Gaps 5;

QY 13 KDGKQTLV-----NPRGVNPTNGVASLSQAG-----VPALKRV 48
DB 138 KGNNEIVVEKKKKSINQNNADIQVNAISLTYPALVKANSELVENQPDVLPVKRDL 197
QY 49 TVSVSPSRKKRYKQVQKQNPACTANGSCDPSVTR-----QVADYTSFTQYSTD 102
DB 198 TISIDLPGMTNDQNKIVK--NATKSNVNAVTLVERWNEKYAQVYPNVS--AKIDYD 252
QY 103 EERAFVETELAA 114
DB 253 DEMAYSESQILIA 264

RESULT 3

US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match 11.5%; Score 76.5; DB 4; Length 409;
Best Local Similarity 25.8%; Pred. No. 0.64;
Matches 34; Conservative 20; Mismatches 53; Indels 25; Gaps 6;

QY 7 TLGNIGKDGKQTLVIN--PR-----GVNPTNGVASLSQAGAVPALERKRVTVSVSOPS 56
DB 109 SLINFKDYRGVGGTRLVNVRNALISFAVNPVDGTPPI-----IAKNQRLITRDLAAG 163
QY 57 RRRKXKXQVQKQNPACTANGSCDPSVTRQAVADYTSFTQYSTDEERAFVTEIAALL 116
DB 164 RFGSN--AIAVIREGFTNNALVPENTAKPYSEITF-----BEVNESVYTIAMMK 213
QY 117 ASPLIDALDOL 128
DB 214 ASKQIIDLPL 225

RESULT 4
US-09-206-942-49
Sequence 49, Application US/09206942
Patent No. 6432669
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
FILE REFERENCE: 1038-861 MIS-1b
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 1073
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-206-942-49

Query Match 11.2%; Score 74; DB 4; Length 1073;
Best Local Similarity 22.8%; Pred. No. 6.2;
Matches 28; Conservative 26; Mismatches 51; Indels 18; Gaps 4;

QY 4 ETVTLGNIGKDGKQTLVINPRG-----VNPNTNGVASLSQAGAVPALERKRVTVSVSQ 54
DB 766 KTLTVGNV--SGNTYTVANRGAULTTLAGSTINGNGVTTSSQSGEIGEVGKTVSVTA 823
QY 55 PSRN--RKNYVQVQKQNPACTANGSCDPSVTRQAVADYTSFTQYSTDEERAFVTE 111
DB 824 TAGSLTVKGAQKINATGATLTASSG---KLTTEASSNITSAGQVDSLQDGSIAQ 879
QY 112 LAA 114
DB 880 ISA 882

RESULT 5

US-09-206-942-47
Sequence 47, Application US/09206942
Patent No. 6432669
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
FILE REFERENCE: 1038-861 MIS-1b
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 1079
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-206-942-47

Query Match 11.2%; Score 74; DB 4; Length 1079;
Best Local Similarity 22.8%; Pred. No. 6.3;
Matches 28; Conservative 26; Mismatches 51; Indels 18; Gaps 4;

QY 4 ETVTLGNIGKDGKQTLVINPRG-----VNPNTNGVASLSQAGAVPALERKRVTVSVSQ 54
DB 772 KTLTVGNV--SGNTYTVANRGAULTTLAGSTINGNGVTTSSQSGEIGEVGKTVSVTA 829
QY 55 PSRN--RKNYVQVQKQNPACTANGSCDPSVTRQAVADYTSFTQYSTDEERAFVTE 111

DB 830 TAGSLTVKGAKNINTEGATITLASSG---KLTTEASSNITSAGQVULSAQDSGIAGQ 885
QY 112 LAA 114
DB 886 ISA 888

RESULT 6

US-09-045-186-2
; Sequence 2, Application US/09045186
; Patent No. 6087154

GENERAL INFORMATION:

APPLICANT: Baez, Melvyn
APPLICANT: Cates, Carolyn A.
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-045-186-2

Query Match 11.1%; Score 73.5; DB 3; Length 383;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVNLPRGVNPTN-----GVA---SLSQAGAVPALERKRVTVSVSOPSRRNKRYKVQVK 67
DB 138 RHQLINRGWRPNRHHAYGVIAVWLVAVASSLFLIYQ--VMTDEPRQN----- 186
QY 68 IONPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFAVTELAAL 115
DB 187 -----VTLDAYKDKYVCVDFPSPDSHRLSYTTLVL 218

RESULT 7

US-08-232-144-4
; Sequence 4, Application US/08232144
; Patent No. 5571695

GENERAL INFORMATION:

APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
APPLICANT: SHINE, John
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, F199, Ernst & Kurz
STREET: 555 13th St, N.W., Suite 701-East

CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,144
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, Barbara G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-107A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-144-4

Query Match 11.1%; Score 73.5; DB 1; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVNLPRGVNPTN-----GVA---SLSQAGAVPALERKRVTVSVSOPSRRNKRYKVQVK 67
DB 138 RHQLINRGWRPNRHHAYGVIAVWLVAVASSLFLIYQ--VMTDEPRQN----- 186
QY 68 IONPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFAVTELAAL 115
DB 187 -----VTLDAYKDKYVCVDFPSPDSHRLSYTTLVL 218

RESULT 8
US-08-555-268A-15
; Sequence 15, Application US/08555268A
; Patent No. 5958709

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Mary
APPLICANT: Branchek, Theresa
APPLICANT: Weinsthank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/DEPTIDE YV/PANCREATIC POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,268A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

```

REFERENCE/DOCKET NUMBER: 44743-Z/JPM/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-555-268A-15

Query Match      11.1%; Score 73.5; DB 2; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4

Oy      16 KQTLVLRGRGNPTN-----GYA--SSQGAVALEKRYTVSVSQSRKRKYQVK 67
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      138 RHQLINRGRPNRRHAYVGIAVTWLAVALSSLPFLYQ--VMDEPFQN----- 186

Oy      68 IONPFACTANGSCDPSYTRQAYADVTFSFTQYSTDEBAFAVTEAL 115
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      187 -----VTLDAIKDKYVCDFDPSPSHSLSTLTLLVL 218


RESULT 9
US-09-200-673-15
Sequence 15, Application US/09200673A
Patent No. 6316203
GENERAL INFORMATION:
APPLICANT: Geisland, Christophe P. G.
APPLICANT: Weinsbank, Richard L.
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypothalamic
FILE REFERENCE: 46166-BZ/JPM
CURRENT FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: 08/566, 096
EARLIER FILING DATE: 1995-12-01
EARLIER APPLICATION NUMBER: 08/349, 025
EARLIER FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-09-200-673-15

Query Match      11.1%; Score 73.5; DB 3; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4

Oy      16 KQTLVLRGRGNPTN-----GYA--SSQGAVALEKRYTVSVSQSRKRKYQVK 67
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      138 RHQLINRGRPNRRHAYVGIAVTWLAVALSSLPFLYQ--VMDEPFQN----- 186

Oy      68 IONPFACTANGSCDPSYTRQAYADVTFSFTQYSTDEBAFAVTEAL 115
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      187 -----VTLDAIKDKYVCDFDPSPSHSLSTLTLLVL 218


RESULT 10
US-10-013-846-4
Sequence 4, Application US/10013846
Patent No. 656367
GENERAL INFORMATION:
APPLICANT: Baktavatchalam, Rajagopal
APPLICANT: Blum, Charles A
```

```

APPLICANT: Brielmann, Harry L
APPLICANT: Darrow, James W
APPLICANT: De Lombaert, Stephane
APPLICANT: Hutchison, Alan
APPLICANT: Tian, Jennifer
APPLICANT: Zheng, Xiaozhang
APPLICANT: Elliott, Richard L
APPLICANT: Hammond, Maryls
TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
TITLE OF INVENTION: 3H-epitroisobenzofuran-1,4'-piperidines
FILE REFERENCE: N00.2001
CURRENT APPLICATION NUMBER: US/10/013.846
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,990
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 384
TYPE: PRT
ORGANISM: homosapiens
US-10-013-846-4

Query Match 11.1%; Score 73.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No.1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

OY 16 KQTLVNPBGVNPNT-----GVA---SISQAGAVPALEKRYTVSVSQPSRNRKRYKQYVK 67
Dh 138 RHQLINPGRGPRPNRRHAYVGIAYIVLAVASSLPFLIYQ--VWTDPEFQK----- 186
OY 68 IQNPFACIANGSCDPSYTRQAYADVTFSFTQYSTDERAPFRTLEAL 115
Dh 187 -----VTLDAKYKDKYVCFPDQPSDSHRLSYTLLILVL 218

RESULT 11
US-09-708-392-9
Sequence 9, Application US/09708392
Patent No. 6734186
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Wayman, Chris
APPLICANT: Maw, G
TITLE OF INVENTION: Pharmaceutical
FILE REFERENCE: PC1043AKM
CURRENT APPLICATION NUMBER: US/09/708,392
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: GB 9926437.6
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: GB 0004021.2
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GB 0013001.3
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 0016563.9
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: GB 0017741.3
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/217,479
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: US 60/221,014
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/221,093
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 384

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TYPE: PRT
ORGANISM: Homo sapiens
US-09-708-392-9

Query Match 11.1%; Score 73.5; DB 4; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGAVPALERKVTYVSQPSRNRKNYKVQK 67
DB 138 RHQLINPRGMRPNRHAYGVIAVWLVAVASSLPFLIQ--VMTDEPFQN----- 186
QY 68 IONPFACTANGSCDPSVTRQAYADVTFSTQYSTDEBRAVFTLEAL 115
DB 187 -----VTLDAYKDKVCFDQPPSDSHRLSYTTLVL 218

RESULT 12

PCT-US93-05039-3
Sequence 3, Application PC/TUS9305039
GENERAL INFORMATION:
APPLICANT: Claes R. Wahlestedt
TITLE OF INVENTION: Human Neuropeptide Y/Peptide YY
TITLE OF INVENTION: Receptor of the Y1-Type and
TITLE OF INVENTION: Antisense Oligonucleotides
TITLE OF INVENTION: Thereto Which Inhibit Vasoconstriction
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05039
FILING DATE: 19930527
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1250
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-05039-3

Query Match 11.1%; Score 73.5; DB 5; Length 384;
Best Local Similarity 25.9%; Pred. No. 1.4;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGAVPALERKVTYVSQPSRNRKNYKVQK 67
DB 138 RHQLINPRGMRPNRHAYGVIAVWLVAVASSLPFLIQ--VMTDEPFQN----- 186
QY 68 IONPFACTANGSCDPSVTRQAYADVTFSTQYSTDEBRAVFTLEAL 115
DB 187 -----VTLDAYKDKVCFDQPPSDSHRLSYTTLVL 218

RESULT 13

US-08-817-869-3
Sequence 3, Application US/08817869
Patent No. 6001970
GENERAL INFORMATION:
APPLICANT: STRADER, CATHERINE D.
APPLICANT: CASCIERI, MARGARET A.
APPLICANT: MACNEIL, DOUGLAS J.
TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM H. NICHOLSON
STREET: 126 EAST LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: US
ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,869
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,017
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: NICHOLSON, WILLIAM H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 19339Y PCT
TELEPHONE: (732) 594-1348
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-869-3

Query Match 11.1%; Score 73.5; DB 3; Length 411;
Best Local Similarity 25.9%; Pred. No. 1.6;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVLPNGVPTN-----GVA---SLSQAGAVPALERKVTYVSQPSRNRKNYKVQK 67
DB 141 RHQLINPRGMRPNRHAYGVIAVWLVAVASSLPFLIQ--VMTDEPFQN----- 189
QY 68 IONPFACTANGSCDPSVTRQAYADVTFSTQYSTDEBRAVFTLEAL 115
DB 190 -----VTLDAYKDKVCFDQPPSDSHRLSYTTLVL 221

RESULT 14

PCT-US95-14377-3
Sequence 3, Application PC/TUS9514377
GENERAL INFORMATION:
APPLICANT: STRADER, CATHERINE D.
APPLICANT: CASCIERI, MARGARET A.
APPLICANT: MACNEIL, DOUGLAS J.
TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APOLLINA
STREET: 126 EAST LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: US
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14377
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/335,017
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: APPOULINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19339Y PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-14377-3

Query Match 11.1%; Score 73.5; DB 5; Length 411;
Best Local Similarity 25.9%; Pred. No. 1.6;
Matches 28; Conservative 12; Mismatches 33; Indels 35; Gaps 4;

QY 16 KQTLVNPBGVNPFN-----GVA---SLSQAGVPALEKRVTVSVQPSNRKNYVQVK 67
DB 141 RHOLIINPRGMRRHAYVGIWVLAIVASSLPLIYQ--VMTDEPFQN----- 189
190 -----VTLDAIKDKYVCFQPSDSHRSLYTLILLVL 221

RESULT 15
US-08-397-411-13
Sequence 13, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: B-specific Antibody Effective to Treat
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-13

Query Match 10.8%; Score 71.5; DB 3; Length 279;
Best Local Similarity 24.0%; Pred. No. 1.5;
Matches 23; Conservative 19; Mismatches 37; Indels 17; Gaps 3;

QY 29 TNGVASLSQAGVPALEKRVTVSVQPSNRKNYVQVKIONPTACTANGSCDP----- 82
DB 179 SSGIYSLSSVTVVPSSISIGTQYICNVNHNKPSNTKVDKVE-PKSCDKHTCPCKCPAG 237
QY 83 --SVTRQAVADTVSFQYSTDEERAFVTELAAL 116
DB 238 GLDTLQAEFD-----QLEDKKSALOTETIANML 265

Search completed: January 4, 2005, 09:35:40
Job time: 11.3622 secs

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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignments)
1450.557 Million cell updates/sec

Title: US-10-622-064-3

Perfect score: 663 1 AKLEVTYIGNIGKDKQTLV.....ALLASPLIDALDQINPAY 132

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications_AA.*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	663	100.0	132	US-10-243-739-10	Sequence 10, Appl
2	663	100.0	132	US-10-244-065-10	Sequence 10, Appl
3	663	100.0	132	US-10-289-454-10	Sequence 10, Appl
4	663	100.0	132	US-10-050-902-159	Sequence 159, App
5	663	100.0	132	US-10-050-898-159	Sequence 159, App
6	663	100.0	132	US-10-346-190-10	Sequence 10, Appl
7	663	100.0	132	US-10-465-811-1	Sequence 10, Appl
8	663	100.0	132	US-10-289-456-10	Sequence 10, Appl
9	663	100.0	132	US-10-622-064-3	Sequence 3, Appl
10	663	100.0	132	US-10-622-124-4	Sequence 4, Appl
11	663	100.0	132	US-10-622-087-4	Sequence 4, Appl
12	663	100.0	132	US-10-243-739-11	Sequence 11, Appl
13	663	100.0	328	US-10-244-065-11	Sequence 11, Appl

14	663	100.0	329	14	US-10-289-454-11	Sequence 11, Appl
15	663	100.0	329	14	US-10-050-902-217	Sequence 217, App
16	663	100.0	329	14	US-10-050-898-217	Sequence 217, App
17	663	100.0	329	14	US-10-346-190-11	Sequence 11, Appl
18	663	100.0	329	15	US-10-465-811-2	Sequence 2, Appl
19	663	100.0	329	15	US-10-289-456-11	Sequence 11, Appl
20	663	100.0	329	15	US-10-622-064-4	Sequence 4, Appl
21	663	100.0	329	15	US-10-622-124-5	Sequence 5, Appl
22	663	100.0	329	16	US-10-622-087-5	Sequence 26, Appl
23	663	98.8	132	14	US-10-243-739-23	Sequence 26, Appl
24	663	98.8	132	14	US-10-243-739-26	Sequence 26, Appl
25	663	98.8	132	14	US-10-244-065-23	Sequence 26, Appl
26	663	98.8	132	14	US-10-244-065-26	Sequence 26, Appl
27	663	98.8	132	14	US-10-289-454-23	Sequence 23, Appl
28	663	98.8	132	14	US-10-289-454-26	Sequence 25, App
29	663	98.8	132	14	US-10-050-902-255	Sequence 25, App
30	663	98.8	132	14	US-10-050-902-259	Sequence 25, App
31	663	98.8	132	14	US-10-050-898-255	Sequence 25, App
32	663	98.8	132	14	US-10-050-898-259	Sequence 25, App
33	663	98.8	132	14	US-10-346-190-23	Sequence 23, Appl
34	663	98.8	132	14	US-10-346-190-26	Sequence 26, Appl
35	663	98.8	132	15	US-10-465-811-14	Sequence 14, Appl
36	663	98.8	132	15	US-10-465-811-17	Sequence 17, Appl
37	663	98.8	132	15	US-10-289-456-23	Sequence 23, Appl
38	663	98.8	132	15	US-10-289-456-26	Sequence 26, Appl
39	663	98.8	132	15	US-10-622-064-6	Sequence 9, Appl
40	663	98.8	132	15	US-10-622-064-9	Sequence 17, Appl
41	663	98.8	132	15	US-10-622-124-17	Sequence 20, Appl
42	663	98.8	132	15	US-10-622-124-20	Sequence 17, Appl
43	663	98.8	132	16	US-10-622-087-17	Sequence 20, Appl
44	663	98.8	132	16	US-10-622-087-20	Sequence 24, Appl
45	663	98.3	132	14	US-10-243-739-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-10-243-739-10
; Sequence 10, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornli, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-10

Query Match	100.0%	Score 663	DB 14	Length 132
Best Local Similarity	100.0%	Pred. No. 1.6e-66		
Matches 132	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 AKLEVTYIGNIGKDKQTLVLPNGVNPNGASISQAGAVPALKRKYVSVSQSRNNK	60		
DB	1 AKLEVTYIGNIGKDKQTLVLPNGVNPNGASISQAGAVPALKRKYVSVSQSRNNK	60		
QY	NYKVQVKIOMPACTANGSCDPSVTRQAVADYTFSTQYSTDEBERAFVTELAALASPL	120		
DB	61 NYKVQVKIOMPACTANGSCDPSVTRQAVADYTFSTQYSTDEBERAFVTELAALASPL	120		
QY	121 LIDAIDQINPAY 132			

Db 121 LIDAIQOLNPAY 132

RESULT 2

US-10-244-065-10
 ; Sequence 10, Application US/10244065
 ; Publication No. US2003009668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin F.
 ; APPLICANT: Storni, Tazio
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Tissot, Alain
 ; APPLICANT: Schwarz, Katrin
 ; APPLICANT: Meijerink, Edwin
 ; APPLICANT: Lipowsky, Gerald
 ; APPLICANT: Bumpens, Paul
 ; APPLICANT: Clelens, Indulis
 ; APPLICANT: Renhofa, Regina
 ; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Partic
 ; FILE REFERENCE: 1700.0220001
 ; CURRENT APPLICATION NUMBER: US/10/244,065
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 60/374,145
 ; PRIOR FILING DATE: 2002-04-22
 ; PRIOR APPLICATION NUMBER: 60/318,994
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage Q-beta
 US-10-244-065-10

Query Match 100.0%; Score 663; DB 14; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.6e-66;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPNGVSLSOAGAVPALERKRVTVSVSOPSRRNK 60
 DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPNGVSLSOAGAVPALERKRVTVSVSOPSRRNK 60
 QY 61 NKVVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
 DB 61 NKVVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132

RESULT 3

US-10-289-454-10
 ; Sequence 10, Application US/10289454
 ; Publication No. US20030157479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Jennige, Gary
 ; APPLICANT: Sonderegger, Ivo
 ; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
 ; FILE REFERENCE: 1700.0360001
 ; CURRENT APPLICATION NUMBER: US/10/289,454
 ; CURRENT FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: US 60/396,636
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: PCT/IB02/00166
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 10/050,902
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/331,045
 ; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 386
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 10
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage Q-beta
 US-10-289-454-10

Query Match 100.0%; Score 663; DB 14; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.6e-66;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPNGVSLSOAGAVPALERKRVTVSVSOPSRRNK 60
 DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPNGVSLSOAGAVPALERKRVTVSVSOPSRRNK 60
 QY 61 NKVVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
 DB 61 NKVVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132

RESULT 4

US-10-050-902-159
 ; Sequence 159, Application US/10050902
 ; Publication No. US20030175290A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Renner, Wolfgang A.
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Tissot, Alain
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Lechner, Franziska
 ; APPLICANT: Seibel, Peter
 ; APPLICANT: Plosek, Christine
 ; TITLE OF INVENTION: Molecular Antigen Array
 ; FILE REFERENCE: 1700.0190004
 ; CURRENT APPLICATION NUMBER: US/10/050,902
 ; CURRENT FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/262,379
 ; PRIOR FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: US 60/288,549
 ; PRIOR FILING DATE: 2001-05-04
 ; PRIOR APPLICATION NUMBER: US 60/326,998
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: US 60/331,045
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 350
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 159
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: Bacteriophage Q Beta
 US-10-050-902-159

Query Match 100.0%; Score 663; DB 14; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.6e-66;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGQTLVLPNGVNPNGVSLSOAGAVPALERKRVTVSVSOPSRRNK 60
 DB 1 AKLEVTTLGNIGDKGQTLVLPNGVNPNGVSLSOAGAVPALERKRVTVSVSOPSRRNK 60
 QY 61 NKVVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
 DB 61 NKVVQVKIONPTACTANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
 QY 121 LIDAIQOLNPAY 132
 DB 121 LIDAIQOLNPAY 132

RESULT 5
US-10-050-898-159
; Sequence 159, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufendiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q Beta
US-10-050-898-159

Query Match 100.0%; Score 663; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGKDKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEBERAFVTELAALLASPL 120
DB 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEBERAFVTELAALLASPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132

RESULT 6
US-10-346-190-10
; Sequence 10, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pellioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-346-190-10

Query Match 100.0%; Score 663; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0;

QY 1 AKLEVTTLGNIGKDKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEBERAFVTELAALLASPL 120
DB 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEBERAFVTELAALLASPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132

RESULT 7
US-10-465-811-1
; Sequence 1, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN P
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS;
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-465-811-1

Query Match 100.0%; Score 663; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0;

QY 1 AKLEVTTLGNIGKDKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 AKLEVTTLGNIGKDKQTLVLPNGVNPPTNGVASISQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEBERAFVTELAALLASPL 120
DB 61 NKVQVKIQNPACTANGSCDPSVTRQAVADVTFSFTQSTDEBERAFVTELAALLASPL 120
QY 121 LIDALDQINPAY 132
DB 121 LIDALDQINPAY 132

RESULT 8
US-10-289-456-10
; Sequence 10, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:

APPLICANT: Bachmann, Martin
APPLICANT: Maurer, Patrick
APPLICANT: Spohn, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289,456
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-289-456-10

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRNK 60
DB 1 AKLEVTTLGNIGDKGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRNK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAYADVTFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQVKIOMPACTANGSCDPSVTRQAYADVTFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 9
US-10-622-064-3
Sequence 3, Application US/10622064
Publication No. US20040059094A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Maurer, Patrick F
TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
FILE REFERENCE: 1700.0300001
CURRENT APPLICATION NUMBER: US/10/622,064
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,575
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Qbeta
US-10-622-064-3

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRNK 60
DB 1 AKLEVTTLGNIGDKGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRNK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAYADVTFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQVKIOMPACTANGSCDPSVTRQAYADVTFSTQYSTDERAFVTELAALLASPL 120

QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 10
US-10-622-124-4
Sequence 4, Application US/106222124
Publication No. US20040076645A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Fulurja, Alma
TITLE OF INVENTION: Gritelin-Carrier Conjugates
FILE REFERENCE: 1700.0340001
CURRENT APPLICATION NUMBER: US/10/622,124
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,638
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-622-124-4

Query Match 100.0%; Score 663; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLEVTTLGNIGDKGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRNK 60
DB 1 AKLEVTTLGNIGDKGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSOPSRRNK 60
QY 61 NYKVQVKIOMPACTANGSCDPSVTRQAYADVTFSTQYSTDERAFVTELAALLASPL 120
DB 61 NYKVQVKIOMPACTANGSCDPSVTRQAYADVTFSTQYSTDERAFVTELAALLASPL 120
QY 121 LIDAIDQLNPAY 132
DB 121 LIDAIDQLNPAY 132

RESULT 11
US-10-622-087-4
Sequence 4, Application US/10622087
Publication No. US20040141984A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F
APPLICANT: Tisseot, Alain
APPLICANT: Ortman, Rainer
APPLICANT: Luond, Rainer
APPLICANT: Staufenbiel, Matthias
TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
FILE REFERENCE: 1700.0350002
CURRENT APPLICATION NUMBER: US/10/622,087
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,639
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/470,432
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-622-087-4

Query Match 100.0%; Score 663; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Db 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
Db 61 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
Qy 121 LIDAIQOLNPAY 132
Db 121 LIDAIQOLNPAY 132

RESULT 12
US-10-243-739-11
; Sequence 11, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-243-739-11

Query Match 100.0%; Score 663; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Db 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 61
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
Db 62 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 121
Qy 121 LIDAIQOLNPAY 132
Db 122 LIDAIQOLNPAY 133

RESULT 13
US-10-244-065-11
; Sequence 11, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tisbet, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meljersink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; TITLE OF INVENTION: Method of Preparation and Use
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
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; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta
US-10-244-065-11

Query Match 100.0%; Score 663; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Db 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 61
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
Db 62 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 121
Qy 121 LIDAIQOLNPAY 132
Db 122 LIDAIQOLNPAY 133

RESULT 14
US-10-289-454-11
; Sequence 11, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Bacteriophage Q-beta CP
US-10-289-454-11

Query Match 100.0%; Score 663; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.5e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Db 2 AKLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 61
Qy 61 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 120
Db 62 NYKVQVKIQNPACTCANGSCDPSVTRQAVADVTFSFTQYSTDEBERAFVTELAALLASPL 121
Qy 121 LIDAIQOLNPAY 132
Db 122 LIDAIQOLNPAY 133
```

RESULT 15
US-10-050-902-217

/ Sequence 217, Application US/10050902
/ Publication No. US20030175290A1

GENERAL INFORMATION:

/ APPLICANT: Renner, Wolfgang A.

/ APPLICANT: Bachmann, Martin

/ APPLICANT: Tissot, Alain

/ APPLICANT: Maurer, Patrick

/ APPLICANT: Lechner, Franziska

/ APPLICANT: Seibel, Peter

/ APPLICANT: Blosek, Christine

/ TITLE OF INVENTION: Molecular Antigen Array

/ FILE REFERENCE: 1700.0190004

/ CURRENT APPLICATION NUMBER: US/10/050,902

/ PRIOR FILING DATE: 2002-01-18

/ PRIOR APPLICATION NUMBER: US 60/262,379

/ PRIOR FILING DATE: 2001-01-19

/ PRIOR APPLICATION NUMBER: US 60/288,549

/ PRIOR FILING DATE: 2001-05-04

/ PRIOR APPLICATION NUMBER: US 60/326,998

/ PRIOR FILING DATE: 2001-10-05

/ PRIOR APPLICATION NUMBER: US 60/331,045

/ PRIOR FILING DATE: 2001-11-07

/ NUMBER OF SEQ ID NOS: 350

/ SOFTWARE: Patentln Ver. 2.1

/ SEQ ID NO 217

/ LENGTH: 329

/ TYPE: PRT

/ ORGANISM: Bacteriophage Q-beta

US-10-050-902-217

Query Match 100.0%; Score 663; DB 14; Length 329;

Best Local Similarity 100.0%; Pred. No. 5.5e-66;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKLETVLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 60

DB 2 AKLETVLGNIGDGKQTLVLPNGVPTNGVASLSQAGAVPALERKVTVSQPSNRK 61

QY 61 NYKVQVKTQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVRTETLALLASPL 120

DB 62 NYKVQVKTQNPACTANGSCDPSVTRQAVADVTFSTQYSTDERAFVRTETLALLASPL 121

QY 121 LIDAIQDLPAY 132

DB 122 LIDAIQDLPAY 133

Search completed: January 4, 2005, 09:41:20

Job time : 33.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 08:56:31 ; Search time 39.6824 Seconds
(without alignments)
1193.281 Million cell updates/sec

Title: US-10-622-064-10
Perfect score: 664
Sequence: 1 ARLEVTVLGNIGKDGRTLV.....ALLASPLLDALDQLNPAV 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	5	ABG94319
2	664	100.0	132	5	ABG80631
3	664	100.0	132	6	ABR56456
4	664	100.0	132	6	ABU09692
5	664	100.0	132	6	ABR44559
6	664	100.0	132	7	ADD24134
7	664	100.0	132	7	ADJ82060
8	664	100.0	132	7	ADK17148
9	664	100.0	132	8	ADJ36317
10	664	100.0	132	8	ADJ67163
11	664	100.0	132	8	ADK52197
12	661	99.5	132	5	ABG94320
13	661	99.5	132	5	ABG80632
14	661	99.5	132	6	ABR56455
15	661	99.5	132	6	ABU09693
16	661	99.5	132	6	ABR44558
17	661	99.5	132	7	ADD24133
18	661	99.5	132	7	ADJ82059
19	661	99.5	132	7	ADK17147
20	661	99.5	132	8	ADJ36316
21	661	99.5	132	8	ADJ67162
22	661	99.5	132	8	ADK52196
23	658	99.1	132	5	ABG94318
24	658	99.1	132	5	ABG80630
25	658	99.1	132	6	ABR56454

26	658	99.1	132	6	ABU09691
27	658	99.1	132	6	ABR44557
28	658	99.1	132	7	ADD24132
29	658	99.1	132	7	ADJ82058
30	658	99.1	132	7	ADK17146
31	658	99.1	132	8	ADJ36315
32	658	99.1	132	8	ADJ67161
33	658	99.1	132	8	ADK52195
34	655	98.6	132	5	ABG94316
35	655	98.6	132	5	ABG80628
36	655	98.6	132	6	ABR56452
37	655	98.6	132	6	ABU09689
38	655	98.6	132	6	ABR44555
39	655	98.6	132	7	ADD24130
40	655	98.6	132	7	ADJ82056
41	655	98.6	132	7	ADK17144
42	655	98.6	132	8	ADJ36313
43	655	98.6	132	8	ADJ67159
44	655	98.6	132	8	ADK52193
45	652	98.2	132	5	ABG94233

ALIGNMENTS

RESULT 1					
ABG94319	ID	ABG94319	standard; protein; 132 AA.		
XX	AC	ABG94319;			
XX	DT	29-AUG-2003 (revised)			
DT	DT	10-DEC-2002 (first entry)			
XX	DE	PQB259 protein.			
XX	KW	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;			
KW	KW	cyclostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;			
KW	KW	vaccine; infectious disease.			
OS	OS	unidentified bacteriophage.			
XX	PN	WO200256905-A2.			
XX	PD	25-JUL-2002.			
XX	PF	21-JAN-2002; 2002MO-IB000166.			
XX	PR	19-JAN-2001; 2001US-0262379P.			
PR	PR	04-MAY-2001; 2001US-0288549P.			
PR	PR	05-OCT-2001; 2001US-0326998P.			
PR	PR	07-NOV-2001; 2001US-0331045P.			
XX	PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.			
XX	PI	Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Seibel P;			
PI	PI	Piossek C;			
XX	DR	WPI; 2002-627351/67.			
XX	PT	Molecular antigen array used in the production of vaccines for infectious diseases.			
PT	PS	Claim 18; Page 146; 441pp; English.			
PS	XX	This invention relates to a novel ordered and repetitive antigen array			
XX	CC	also in the production of vaccines for infectious diseases. The invention			
CC	CC	also discloses a composition comprising a non-natural molecular scaffold			
CC	CC	comprising a core particle selected from a core particle of a non-natural			
CC	CC	origin and a core particle of natural origin and an organism comprising			
CC	CC	at least one first attachment site, where the organism is connected to			
CC	CC	the core particle by at least one covalent bond. Also disclosed is an			
CC	CC	antigen or antigenic determinant with at least one second attachment			

CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (Abeta1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Qbeta coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, anti-allergic, immunomodulatory, cytostatic,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;

Best Local Similarity 100.0%; Pred. No. 2e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60

DB 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60

QY 61 NKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120

DB 61 NKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

RESULT 2
 ABG80631
 ID ABG80631 standard; protein; 132 AA.

XX ABG80631;

XX 29-NOV-2002 (first entry)

DB Bacteriophage Q-beta A1 coat protein mutant Qbeta-251.

XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; Influenza;
 KW graft versus host disease; Igg-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.

OS Bacteriophage Qbeta.
 OS Synthetic.

PN WO200256907-A2.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002MO-IB000168.

XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326988P.
 PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEB/) LUEBEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 PI Maurer P., Lechner F., Ortmann R., Luebend R., Staufenbiel M., Frey P;
 PI Renner WA, Bachmann M, Tissot A, Seibel P, Plosek C;
 XX WPI, 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for infectious
 XX diseases.

PS Example 18; Page 403; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural
 XX molecular scaffold comprising: (i) a core particle selected from: (1) a
 XX core particle of a non-natural origin; and (2) a core particle of natural
 XX origin; and (ii) an organiser comprising at least one first attachment
 XX site, where the organiser is connected to the core particle by at least
 XX one covalent bond; (b) an antigen or antigenic determinant with at least
 XX one second attachment site, where the antigen or antigenic determinant is
 XX amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 XX attachment site is selected from: (i) an attachment site not naturally
 XX occurring with the antigen or antigenic determinant; and (ii) an
 XX attachment site naturally occurring with the antigen or antigenic
 XX determinant, where the second attachment site is capable of association
 XX through at least one non-peptide bond to the first attachment site; and
 XX where the antigen or antigenic determinant and the scaffold interact
 XX through the association to form an ordered and repetitive antigen array.
 XX Also included is a process for producing a non-naturally occurring
 XX ordered and repetitive antigen array. The composition is used in
 XX immunisation and as a vaccine for diseases such as influenza, graft
 XX versus host disease, Igg-mediated allergic reactions, anaphylaxis, adult
 XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 XX gravis, immunoproliferative disease lymphadenopathy,
 XX angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 XX osteoporosis and infectious diseases. The antigens are modified to possess
 XX a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
 XX or C-terminal linker peptide which serves as the attachment point to a
 XX virus like particle or bacterial protein (the scaffold protein). The
 XX present sequence is bacterial protein or peptide which is coupled to the
 XX modified antigen to form the molecular antigen array

SO Sequence 132 AA;

Query Match 100.0%; Score 664; DB 5; Length 132;

Best Local Similarity 100.0%; Pred. No. 2e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60

DB 1 ARLEVTTLGNIGKDGKQTLVLPNGVNPPTNGVASLSQAGAVPALKRRVTVSVSOPSRRNK 60

QY 61 NKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120

DB 61 NKVQVKIQNPACTANGSCDPSVTRKXADVTFSFTQYSTDEERAFVTELAALLASPL 120

QY 121 LIDAIDQINPAY 132

DB 121 LIDAIDQINPAY 132

RESULT 3
 ABR56456
 ID ABR56456 standard; protein; 132 AA.

XX ABR56456;
AC
XX 28-JUN-2003 (first entry)
DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:27.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KW cytosolic; virucide; antibacterial; antiparasitic; fungicide;
KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KW inflammatory autoimmune disease.
XX Bacteriophage Qbeta.
OS Synthetic.
XX
XX WO2003024480-A2.
XX
XX 27-MAR-2003.
XX
XX 16-SEP-2002; 2002WO-IB004252.
XX PF
XX 14-SEP-2001; 2001US-0318967P.
XX PR
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA
XX Bachmann M, Storni T, Lechner F;
XX
XX WPI, 2003-363095/34.
XX DR
XX
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX Disclosure; Page 183; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumors and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ARLEVTTLGNIGKGRQTLVLNPRGVNPTNGVASLSQAGAVPALERKVTVSQPSRRNK 60

DB 1 ARLEVTTLGNIGKGRQTLVLNPRGVNPTNGVASLSQAGAVPALERKVTVSQPSRRNK 60
QY 61 NYKVQVKIQLNPACTANGSCDPSVTROKADVTSGFTQYSTDEERAFRTETLALIASPL 120
DB 61 NYKVQVKIQLNPACTANGSCDPSVTROKADVTSGFTQYSTDEERAFRTETLALIASPL 120
QY 121 LIDAIQQLNPAY 132
DB 121 LIDAIQQLNPAY 132
RESULT 4
ABU09692
ID ABU09692 standard; protein; 132 AA.
XX
XX ABU09692;
AC
XX
XX 03-JUN-2003 (first entry)
XX
XX Bacteriophage Qbeta mutant coat protein #4.
XX
XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
KW cardiast; nephrotropic; ophthalmological; immunostimulant; vaccine;
KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KW renin-activated angiotensin system; hypertension; stroke; infarction;
KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
KW mutin.
XX
XX Bacteriophage Qbeta.
OS
XX
XX WO2003031466-A2.
XX PN
XX
XX 17-APR-2003.
XX PD
XX
XX 07-OCT-2002; 2002WO-EP011219.
XX PF
XX
XX 05-OCT-2001; 2001US-0326998P.
XX PR
XX 18-JAN-2002; 2002US-00050902.
XX PR
XX 21-JAN-2002; 2002WO-IB000166.
XX PR
XX 19-JUN-2002; 2002US-0396637P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA
XX Bachmann M;
XX
XX WPI, 2003-430264/40.
XX DR
XX
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety, useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
XX
XX Claim 20; Page 94; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate
CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal
CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC mutant bacteriophage Qbeta coat protein used in the preparation of the
CC vaccine conjugates of the invention
XX
XX Sequence 132 AA;
SQ

Query Match 100.0%; Score 664; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;

Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEVTTLGNIGKDGROTLVLPNGVNPNGVNSISQAGAVPALERKRVTVSVSOPSRRNK 60
 DB 1 ALEVTTLGNIGKDGROTLVLPNGVNPNGVNSISQAGAVPALERKRVTVSVSOPSRRNK 60

QY 61 NKVVQVKIÖNPACTRANGSCDPSVTRÖKYADVTFSTQYSTDEERAFVTELAALLASPL 120
 DB 61 NKVVQVKIÖNPACTRANGSCDPSVTRÖKYADVTFSTQYSTDEERAFVTELAALLASPL 120

QY 121 LIDAIDQÖLPAY 132
 DB 121 LIDAIDQÖLPAY 132

RESULT 5
 ABR44559
 ID ABR44559 standard; protein; 132 AA.
 AC ABR44559;
 DT 25-JUL-2003 (first entry)
 XX
 DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:27.

XX Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

OS Bacteriophage Qbeta.
 OS Synthetic.
 PN WO2003024481-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 16-SEP-2002; 2002WO-IB004132.
 XX
 PR 14-SEP-2001; 2001US-0318994P.
 PR 22-APR-2002; 2002US-0374145P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (MAURER P. MAURER P.
 PA (TISSOT A. TISSOT A.
 PA (SCHWAB K. SCHWAB K.
 PA (MEIJER E. MEIJER E.
 PA (LIPOWSKY G. LIPOWSKY G.
 PA (PUMPER P. PUMPER P.
 PA (CIELENS I. CIELENS I.
 PA (RENNHOFER R. RENNHOFER R.

PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielens I, Renhofa R, Bachmann M, Storni T;
 XX
 DR WPI; 2003-354564/33.
 XX
 PT New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX
 PS Disclosure; Page 262; 322pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing an immune response in an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or

CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC printing a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the vaccine;
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (I) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumors (e.g. breast cancer,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 CC

SEQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEVTTLGNIGKDGROTLVLPNGVNPNGVNSISQAGAVPALERKRVTVSVSOPSRRNK 60
 DB 1 ALEVTTLGNIGKDGROTLVLPNGVNPNGVNSISQAGAVPALERKRVTVSVSOPSRRNK 60

QY 61 NKVVQVKIÖNPACTRANGSCDPSVTRÖKYADVTFSTQYSTDEERAFVTELAALLASPL 120
 DB 61 NKVVQVKIÖNPACTRANGSCDPSVTRÖKYADVTFSTQYSTDEERAFVTELAALLASPL 120

QY 121 LIDAIDQÖLPAY 132
 DB 121 LIDAIDQÖLPAY 132

RESULT 6
 ADD24134
 ID ADD24134 standard; protein; 132 AA.
 XX
 AC ADD24134;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Bacteriophage Qbeta coat protein mutant Qbeta-259.
 XX
 KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; coat protein; mutant; mutein.
 XX
 OS Synthetic.
 OS Bacteriophage Qbeta.
 PN WO2003059386-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-BP000460.
 XX
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (BAACHMANN M. MAURER P, PELLICOLI E, RENNER W;
 PI Bachmann M, Maurer P, Pellicoli E, Renner W;
 XX
 DR WPI; 2003-598483/56.
 XX
 PT A vaccine composition for preventing or treating prion diseases (e.g.

Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-phage) and at least one prion protein or peptide bound to the virus-like particle.

Example 1; SEQ ID NO 27; 246pp; English.

This invention relates to a novel vaccine composition comprising a virus-like or a core particle with at least one first attachment site and at least one antigen or antigenic determinant that is a prion protein (Prp) or its dimer, or a Prp peptide, the antigen or antigenic determinant being bound to the virus-like or core particle. The vaccine of the invention may have neuroprotective or antiinflammatory activity. The composition is useful as a medicament or in manufacturing a medicament for the treatment or prevention of prion diseases. The prion diseases may include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob Disease. The present sequence is the amino acid sequence of a mutant coat protein from bacteriophage Obeta which may be used during the creation of the vaccine composition of the invention.

Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKQVQKIQNPACTRANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NKQVQKIQNPACTRANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 7
ADJ82060
ID ADJ82060 standard; protein; 132 AA.

AC ADJ82060;
DT 06-MAY-2004 (first entry)
DE Protein for RANKL antigen array to treat bone disease.
KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
KW bone disease; encephalopathy; immune system stimulation.
XX Unidentified.
OS
XX WO2003039225-A2.
FN
XX 15-MAY-2003.
PD
XX 07-NOV-2002; 2002WO-EP012449.
PF
XX 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann M, Maurer P, Spohn G;
XX
DR WPI; 2003-441430/41.
XX
PT New compositions comprising a core particle and at least one antigen or
PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
PT of bone diseases, particularly mammalian encephalopathies.

XX Disclosure; SEQ ID NO 27; 222pp; English.

XX The invention relates to a composition comprising a core particle having
XX at least one first attachment site, and at least one antigen or antigenic
XX determinant having at least one second attachment site. The antigen or
XX antigenic determinant is a RANKL protein, RANKL fragment or RANKL
XX peptide. The second attachment site is (non-) naturally occurring with
XX the antigen or antigenic determinant, and is capable of association to
XX the first attachment site. The antigen or antigenic determinant and the
XX core particle interact through the association to form an ordered and
XX repetitive antigen array. The composition is useful as a medicament, or
XX for the manufacture of a medicament for treating bone diseases. The
XX composition is especially useful for as a vaccine for therapy or
XX prophylaxis of bone diseases, particularly mammalian encephalopathies,
XX and for stimulating mammalian immune system. This sequence represents a
XX protein of the invention.

Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
DB 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
QY 61 NKQVQKIQNPACTRANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NKQVQKIQNPACTRANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQINPAY 132
DB 121 LIDAIDQINPAY 132

RESULT 8
ADK17148
ID ADK17148 standard; peptide; 132 AA.

AC ADK17148;
DT 06-MAY-2004 (first entry)
DE Virus-like particle repetitive antigen array peptide #27.
KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;
KW interleukin; IL-5; IL-13; ectaxin; repetitive antigen array;
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
XX Unidentified.
OS
XX WO2003040164-A2.
FN
XX 15-MAY-2003.
PD
XX 07-NOV-2002; 2002WO-EP012455.
PF
XX 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-1B000166.
PR 19-JUL-2002; 2002US-0396635P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Bachmann M, Jennings G, Sonderregger I;
XX
DR WPI; 2003-441518/41.
XX
PT Composition comprising an ordered and repetitive antigen or antigenic
PT determinant array, useful as a medicament, or for manufacturing a
PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or

PT Hodgkin's Lymphoma.

XX Disclosure; SEQ ID NO 27; 245pp; English.

XX
PS
CC The invention relates to a composition comprising a virus-like particle
CC and at least one antigen, which is a protein or peptide of interleukin
CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC core particle with at least one first attachment site and at least one
CC antigen with at least one second attachment site, where the antigen is a
CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC is an attachment site naturally or not naturally occurring with the
CC antigen or antigenic determinant. The second attachment site is capable
CC of association to the first attachment site, and where the antigen or
CC antigenic determinant and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC compositions are useful as medicaments, or for manufacturing a medicament
CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
CC Hodgkin's lymphoma and related diseases. This sequence is used to
CC generate the compound of the invention.

XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTYIGNIGKDGROTLVLPNGVNPNGVSLISQAGAVPALEKRYTVSVSQPSRNRK 60

DB 1 ARLEVTYIGNIGKDGROTLVLPNGVNPNGVSLISQAGAVPALEKRYTVSVSQPSRNRK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTLEAALLASPL 120

DB 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTLEAALLASPL 120

QY 121 LIDAIQOLNPAY 132

DB 121 LIDAIQOLNPAY 132

QY

DB RESULT 9
ADJ36317
ID ADJ36317 standard; protein; 132 AA.

AC ADJ36317;

XX 22-APR-2004 (first entry)

DE Bacteriophage Qbeta coat protein virus-like particle mutant K2RKL6R.

XX antiallergic; cytostatic; virucide; immunostimulant; vaccine;
KM immune response; virus-like particle; immunostimulatory; allergy; tumour;
KM chronic disease; chronic viral disease; bacteriophage Qbeta;
KM coat protein; VLP; adjuvant; mutant; mutein.

XX Bacteriophage Qbeta.

XX WO2004000351-A1.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-EP006541.

XX 20-JUN-2002; 2002US-0389898P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachman MF, Renner WA;

XX WPI; 2004-108361/11.

XX
PT New compositions comprising a virus-like particle (VLP), an
PT immunostimulatory substance bound to the VLP, and an antigen mixed with
PT the VLP, useful for enhancing immune response or for treating e.g. tumors

PT or chronic viral diseases.

XX Disclosure; SEQ ID NO 18; 252pp; English.

XX
PS
CC The invention describes a composition for enhancing an immune response in
CC an animal comprising a virus-like particle, an immunostimulatory
CC substance bound to the virus-like particle, and an antigen mixed with the
CC virus-like particle. The composition or the vaccine is useful in the
CC manufacture of a pharmaceutical for the treatment of a disorder or
CC disease such as allergies, tumours, chronic diseases and chronic viral
CC diseases. The composition is also useful for enhancing an immune response
CC in an animal. This is the amino acid sequence of a bacteriophage Qbeta
CC coat protein mutant, a virus like particle (VLP) that can be used in the
CC adjuvant of the invention.

XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTYIGNIGKDGROTLVLPNGVNPNGVSLISQAGAVPALEKRYTVSVSQPSRNRK 60

DB 1 ARLEVTYIGNIGKDGROTLVLPNGVNPNGVSLISQAGAVPALEKRYTVSVSQPSRNRK 60

QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTLEAALLASPL 120

DB 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVRTLEAALLASPL 120

QY 121 LIDAIQOLNPAY 132

DB 121 LIDAIQOLNPAY 132

QY

DB RESULT 10
ADJ67163
ID ADJ67163 standard; protein; 132 AA.

AC ADJ67163;

XX 06-MAY-2004 (first entry)

DE Phage Qbeta coat protein mutant Qbeta 259 for antigen display array.

XX anorectic; core particle; antigenic determinant; ghrelin; P-pillin;
KM antigenic array.

XX Bacteriophage Qbeta.

XX Synthetic.

XX WO2004009124-A2.

XX 29-JAN-2004.

XX 18-JUL-2003; 2003WO-EP007849.

XX 19-JUL-2002; 2002US-0396638P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann MF, Fulurija A;

XX WPI; 2004-132866/13.

XX
PT New composition comprising a core particle having a first attachment site
PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
PT peptide having a second attachment site, useful for treating obesity.

XX Disclosure; SEQ ID NO 21; 175pp; English.

XX
CC The invention relates to a new composition comprising: (1) a core
CC particle with at least one first attachment site; and (1i) at least one
CC antigen or antigenic determinant with at least one second attachment

CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
CC peptide, and where the second attachment site being consisting of an
CC attachment site not naturally occurring with the antigen or antigenic
CC determinant and an attachment site naturally occurring with the antigen
CC or antigenic determinant, where the second attachment site is capable of
CC association to the first attachment site, and where the ghrelin or a
CC ghrelin peptide and the core particle interact through the association to
CC form an ordered and repetitive antigen array. The composition is useful
CC for treating obesity. The repetitive array may form part of a phage or
CC bacterial display array. This peptide corresponds to a Bacteriophage
CC Obeta coat protein mutant which can used as part of the repetitive or
CC antigenic array.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSOPSRRNK 60

DB 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSOPSRRNK 60

QY 61 NYKVQVKIÖNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBERAFRTTELAALLASPL 120

DB 61 NYKVQVKIÖNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBERAFRTTELAALLASPL 120

QY 121 LIDAIDQLNPAV 132

DB 121 LIDAIDQLNPAV 132

RESULT 11

ADKS2197

ID ADKS2197 standard; protein; 132 AA.

XX ADKS2197;

DT 20-MAY-2004 (first entry)

DE Bacteriophage Obeta coat protein mutant K2R K16R.

XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;

KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;

XX coat protein; CP; mutant; mutein.

OS Bacteriophage Obeta.

XX Synthetic.

Key Location/Qualifiers

FT Misc-difference 2 /note= "Wild type Lys substituted by Arg"

FT Misc-difference 16 /note= "Wild type Lys substituted by Arg"

PN WO2004016282-A1.

XX 26-FEB-2004.

PF 18-JUL-2003; 2003WO-EP007864.

PR 19-JUL-2002; 2002US-0396639P.

PR 15-MAY-2003; 2003US-0470432P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI (NOVS) NOVARTIS PHARMA AG.

XX Bachmann MF, Tisot A, Ortmann R, Luesend R, Straufenbiel M;

XX Frey P;

XX WPI; 2004-203731/19.

Composition comprising a core particle with at least one attachment site,

PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases

XX such as Alzheimer's disease.

PS Example 1; SEQ ID NO 21; 184pp; English.

CC The invention describes a novel composition comprising a virus-like core
CC particle with at least one attachment site, and an antigenic amyloid beta
CC 1-6 peptide. The new composition comprises: a core particle with at least
CC one first attachment site; and at least one antigen or antigenic
CC determinant with at least one second attachment site, where the antigen
CC or antigenic determinant is a Amyloid beta 1-6 peptide, and where the
CC second attachment site comprises: an attachment site not naturally
CC occurring with the antigen or antigenic determinant; or an attachment
CC site naturally occurring with the antigen or antigenic determinant. The
CC second attachment site is capable of association to the first attachment
CC site and the beta 1-6 peptide and the core particle interact through the
CC association to form an ordered and repetitive antigen array. The
CC composition is useful for the manufacture of a medicament for treating
CC Alzheimer's disease and related diseases. This is the amino acid sequence
CC of an RNA bacteriophage Obeta coat protein mutant that can be used in the
CC preparation of the compositions and vaccines of the invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 664; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 2e-71; Mismatches 0; Gaps 0;

Matches 132; Conservative 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSOPSRRNK 60

DB 1 ARLEVTLTGNIGKDGKQRTLVLPNGVNPPTNGVASLSQAGAVPALEKRYTVSVSOPSRRNK 60

QY 61 NYKVQVKIÖNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBERAFRTTELAALLASPL 120

DB 61 NYKVQVKIÖNPACTANGSCDPSVTROKXADVTFSFTQYSTDEBERAFRTTELAALLASPL 120

QY 121 LIDAIDQLNPAV 132

DB 121 LIDAIDQLNPAV 132

RESULT 12

ABG94320

ID ABG94320 standard; protein; 132 AA.

XX ABG94320;

DT 29-AUG-2003 (revised)

DT 10-DEC-2002 (first entry)

DE PQB251 protein.

XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;

KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;

XX vaccine; infectious disease.

OS unidentified bacteriophage.

XX WO200256905-A2.

PD 25-JUL-2002.

PF 21-JAN-2002; 2002WO-1B000166.

PR 19-JAN-2001; 2001US-0262379P.

PR 04-MAY-2001; 2001US-0286549P.

PR 05-OCT-2001; 2001US-032698P.

PR 07-NOV-2001; 2001US-0331045P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Renner WA, Bachmann M, Tisot A, Maurer P, Lechner F, Seibel P;

XX Plosek C;

XX WPI; 2002-627351/67.
 XX Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX Claim 18; Page 426; 441pp; English.
 XX
 CC This invention relates to a novel ordered and repetitive antigen array
 CC used in the production of vaccines for infectious diseases. The invention
 CC also discloses a composition comprising a non-natural molecular scaffold
 CC comprising a core particle selected from a core particle of a non-natural
 CC origin and a core particle of natural origin and an organiser comprising
 CC at least one first attachment site, where the organiser is connected to
 CC the core particle by at least one covalent bond. Also disclosed is an
 CC antigen or antigenic determinant with at least one second attachment
 CC site, where the antigen or antigenic determinant is amyloid beta peptide
 CC (A β 1-42) or its fragment and where the second attachment site is
 CC selected from an attachment site not naturally occurring with the antigen
 CC or antigenic determinant and an attachment site naturally occurring with
 CC the antigen or antigenic determinant, where the second attachment site is
 CC capable of association through at least one non-peptide bond to the first
 CC attachment site and where the antigen or antigenic determinant and the
 CC scaffold interact through the association to form an ordered and
 CC repetitive antigen array. The invention also comprises a coat protein
 CC capable of forming a capsid which comprises mutant Q β coat proteins
 CC having an amino acid sequence selected from five amino acid sequences
 CC fully defined in the specification. The compounds of the invention may
 CC have antimicrobial, anti-allergic, immunomodulatory, cytoprotective,
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
 CC immunisation and as a vaccine. The present sequence represents a protein
 CC sequence used to create the compositions of the invention. (Updated on 29
 CC -AUG-2003 to standardise OS field)
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 4.5e-71;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLETVTLNIGKDGQTLVLRNVPNNGVSLSOAGVPLAEKRVTVSVQSPRNK 60
 Db 1 AKLEIVTLNIGKDGQTLVLRNVPNNGVSLSOAGVPLAEKRVTVSVQSPRNK 60
 QY 61 NYKQVQKIQNPACTANGSCDPSVTRQKADVTFSFQVSTDEBERAFVETELAAALASP 120
 Db 61 NYKQVQKIQNPACTANGSCDPSVTRQKADVTFSFQVSTDEBERAFVETELAAALASP 120
 QY 121 LIDAIQOLNPAY 132
 Db 121 LIDAIQOLNPAY 132
 QY 121 LIDAIQOLNPAY 132
 Db 121 LIDAIQOLNPAY 132
 RESULT 13
 ABG80632
 ID ABG80632 standard; protein; 132 AA.
 AC ABG80632;
 XX
 XX 29-NOV-2002 (first entry)
 XX
 DE Bacteriophage Q-beta A1 coat protein mutant Qbeta-259.
 XX
 XX Molecular antigen array; vaccine; antigen; antimicrobial;
 KM molecular scaffold; amyloid beta; A β 1-42; influenza;
 KM graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease; lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;

KW enterokinase; cysteine-containing linker.
 XX
 OS Bacteriophage Qbeta.
 OS Synthetic.
 XX
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 XX 21-JAN-2002; 2002WO-1B000168.
 PF
 XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTW/) ORTMANN R.
 PA (LUBO/) LUBOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P., Lechner F., Ortmann R., Lueoend R., Staufenbiel M., Frey P;
 PI Renner WA., Bachmann M., Tissot A., Sebbel P., Ploessek C;
 XX
 XX WPI; 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 PS Example 18; Page 146; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (A β 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The antigens are modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein). The
 CC present sequence is bacterial protein or peptide which is coupled to the
 CC modified antigen to form the molecular antigen array
 XX
 SQ Sequence 132 AA;
 Query Match 99.5%; Score 661; DB 5; Length 132;
 Best Local Similarity 99.2%; Pred. No. 4.5e-71;
 Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARLEVTYIGNIGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Db 1 AKLEVTYIGNIGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Qy 61 NYKQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Db 61 NYKQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Qy 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 14
ABR56455
ID ABR56455 standard; protein; 132 AA.
AC ABR56455;
XX 28-JUL-2003 (first entry)
DE Bacteriophage Q-beta coat protein mutant SEQ ID NO:26.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KM cytostatic; virucide; antibacterial; antiparasitic; fungicide;
KM antiallergic; immunosuppressive; antidiabetic; antiinflammatory;
KM antihydroid; antidiabetic; neuroprotective; nootropic; osteoporotic;
KM antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KM anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KM graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KM Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KM inflammatory autoimmune disease.
XX
XX Bacteriophage Qbeta.
OS Synthetic.
OS WO2003024480-A2.
XX
XX 27-MAR-2003.
XX
XX 16-SEP-2002; 2002MO-IB004252.
XX
XX 14-SEP-2001; 2001US-0318967P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann MF, Storni T, Lechner F;
PI WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX Disclosure; Page 182; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antidiabetic, antiinflammatory,
CC antihydroid, antidiabetic, neuroprotective, nootropic, osteoporotic,
CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an

CC animal, enhancing anti-viral protection in an animal, or immunizing or
CC treating tumors and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69852 to ACC69852 and ABR56401 to ABR56509
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 132 AA;
SQ
Query Match 99.5%; Score 661; DB 6; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.5e-71;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ARLEVTYIGNIGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Db 1 AKLEVTYIGNIGKDGKQRTLVNPRGVNPTNGVASLSQAGAVPALERKRVTVSVSOPSRRNK 60
Qy 61 NYKQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Db 61 NYKQVKIQNPACTANGSCDPSVTRQKXADVTFSFTQYSTDEBRAFPRTTELAALLASPL 120
Qy 121 LIDAIDQINPAY 132
Db 121 LIDAIDQINPAY 132
RESULT 15
ABU09693
ID ABU09693 standard; protein; 132 AA.
XX
XX ABU09693;
XX
XX 03-JUL-2003 (first entry)
XX
XX Bacteriophage Qbeta mutant coat protein #5.
DE Bacteriophage Qbeta mutant coat protein #5.
XX
XX Bacteriophage Qbeta; coat protein; hypotensive; cerebroprotective;
KM cardiant; nephroprotective; ophthalmological; immunostimulant; vaccine;
KM angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KM renin-activated angiotensin system; hypertension; stroke; infarction;
KM congestive heart failure; kidney failure; retinal haemorrhage; mutant;
KM mutein.
XX
XX Bacteriophage Qbeta.
OS
XX
XX WO2003031466-A2.
XX
XX 17-APR-2003.
XX
XX 07-OCT-2002; 2002MO-BP011219.
XX
XX 05-OCT-2001; 2001US-0326998P.
XX
XX 07-NOV-2001; 2001US-0331045P.
XX
XX 18-JAN-2002; 2002US-00050902.
XX
XX 21-JAN-2002; 2002MO-IB000156.
XX
XX 19-JUL-2002; 2002US-0396637P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M;
PI WPI; 2003-430264/40.
XX
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety, useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
XX
XX Claim 20; Page 94; 97pp; English.
XX
XX The invention describes an angiotensin peptide moiety carrier conjugate

comprising: (a) a carrier with at least one first attachment site; and (b) at least one angiotensin peptide moiety with at least one second attachment site. The angiotensin peptide conjugate and compositions comprising them are useful for immunising an animal against an angiotensin peptide, and for treating or preventing a physical disorder associated with renin-activated angiotensin system such as hypertension, stroke, infarction, congestive heart failure, kidney failure, and retinal haemorrhage. The conjugate is also useful for inducing immune responses, including producing antibodies. This is the amino acid sequence of a mutant bacteriophage Qbeta coat protein used in the preparation of the vaccine conjugates of the invention

XX
SQ Sequence 132 AA:

Query Match 99.5%; Score 661; DB 6; Length 132;

Best Local Similarity 99.2%; Pred. No. 4.5e-71;

Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	ARLEVTTLGNIGKDGROTILVLPNGVNPPTNGVASLSQAGAVPALERKVTVSVSQPSRNK	60
Db	1	AKLEIVTLGNIGKDGROTILVLPNGVNPPTNGVASLSQAGAVPALERKVTVSVSQPSRNK	60
QY	61	NYKVQVKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAAVRTTELALIASPL	120
Db	61	NYKVQVKIQNPFTACTANGSCDPSVTRQKADVTFSFTQYSTDERAAVRTTELALIASPL	120
QY	121	LIDAIQQLNPAY	132
Db	121	LIDAIQQLNPAY	132

Search completed: January 4, 2005, 09:11:02
Job time : 39.6824 secs

FILE REFERENCE: 100564-00079
CURRENT APPLICATION NUMBER: US/09/948,722
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/485,717
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/EP98/05109
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: EP 97/114,614.7
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysomal
OTHER INFORMATION: escape domain
US-09-948-722-2

Query Match 12.7%; Score 84.5; DB 4; Length 626;
Best Local Similarity 22.7%; Pred. No. 0.16; Mismatches 44; Indels 35; Gaps 5;
Matches 30; Conservative 23;

QY 13 KCGRQTLV-----NPRGVNPTNGVASLSQAGA-----VPALEKRV 48
DB 138 KCGNEIVVEKKKKSNONNADQVNNALISLTPGALVKANSEIVENQPDVLPVGRDGL 197
QY 49 TVSVSOPSRNRKRYKQVQKIQNFTACTANGSCDPSVTR-----QKYADVTSTFOYSTD 102
DB 198 TISIDIPGWTNQNOKIVK--NATKSNVNNVAVTLVERNMEKXAQAYPNVS--AKIDYD 252
QY 103 EERAFVTELEA 114
DB 253 DEMAYSESQLIA 264

RESULT 3

US-09-328-352-4249
Sequence 4249, Application US/09328352
Patent No. 6562938
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4249
LENGTH: 409
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4249

Query Match 12.0%; Score 79.5; DB 4; Length 409;
Best Local Similarity 26.5%; Pred. No. 0.35; Mismatches 53; Indels 25; Gaps 6;
Matches 35; Conservative 19;

QY 7 TLGNIGKDGQTLVNL--PR-----GVNPTNGVASLSQAGVPALEKRVTV-SVSQPS 56
DB 109 SLINFTKDVAGGTRLVNVRNRLALISFAVNPVGTTP-----IAKNORLITRDLAAG 163
QY 57 RNKNKRVQKIQNFTACTANGSCDPSVTRQKXADVTSTFOYSTDBEARFVTELEA 116
DB 164 RTGSN--ALAYIRETGFNNALVPENTAKPYSEITF-----BEVWESVTIAHMLK 213
QY 117 ASPLLDIAIDQL 128
DB 214 ASKQIIDDLPQL 225

RESULT 4
US-09-252-991A-23637
Sequence 23637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23637
LENGTH: 916
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23637

Query Match 11.2%; Score 74.5; DB 4; Length 916;
Best Local Similarity 23.7%; Pred. No. 5.3; Mismatches 53; Indels 21; Gaps 4;
Matches 28; Conservative 16;

QY 9 GNIGKDG-----RQTLVNPGRVNPNGVASLSQAGVPALEKRVTVSVS-----QP 55
DB 789 GLGGEGALARRAALVQARRIDPFGGLAALPVGGPDALEQADPAFGSLDQRWQA 848
QY 56 SNNRKYKQVQKIQNFTAC--TANGSCDPSVTRQKXADVTSTFOYSTDBEARFV 110
DB 849 BERGAETRAQESAREHREPCRSIEANADCEPLSDAGKW-----PWTTFDSATRMALRT 901

RESULT 5

US-09-045-186-2
Sequence 2, Application US/09045186
Patent No. 6087154
GENERAL INFORMATION:
APPLICANT: Baez, Melvyn
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,186
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11376
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-045-186-2

Query Match 10.8%; Score 71.5; DB 3; Length 383;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLLINPRGVNPTN-----GVA-----SLSQAGAVPALEKRVTVSVSOPSRRNKRYKVQVK 67
DB 138 RHQLLINPRGWRPNRHHAYVGIWVLAIVASSLPFLIYQ--VMTDEPRQN----- 186
QY 68 IONPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAAL 115
DB 187 -----VTLDAYKDKYVCFDQPPSDSHRLSYTTLTLVL 218

RESULT 6

US-08-232-144-4
Sequence 4, Application US/08232144
Patent No. 5571695

GENERAL INFORMATION:

APPLICANT: SELBIE, Lisa

APPLICANT: HERZOG, Herbert

TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figs, Ernst & Kurz

STREET: 555 13th St, N.W., Suite 701-East

CITY: Washington

STATE: DC

COUNTRY: US

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,144

FILING DATE: 26-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, Barbara G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1871-107A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-232-144-4

Query Match 10.8%; Score 71.5; DB 1; Length 384;

Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLLINPRGVNPTN-----GVA-----SLSQAGAVPALEKRVTVSVSOPSRRNKRYKVQVK 67
DB 138 RHQLLINPRGWRPNRHHAYVGIWVLAIVASSLPFLIYQ--VMTDEPRQN----- 186
QY 68 IONPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAAL 115
DB 187 -----VTLDAYKDKYVCFDQPPSDSHRLSYTTLTLVL 218

RESULT 7

US-08-555-268A-15
Sequence 15, Application US/08555268A
Patent No. 5958709

GENERAL INFORMATION:

APPLICANT: Baird, Jonathan A.

APPLICANT: Walker, Mary

APPLICANT: Branchek, Theresa

APPLICANT: Weinshank, Richard L.

TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE

TITLE OF INVENTION: Y/PEPTIDE Y1/PANCREATIC POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/555,268A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 44743-Z/JPW/MAT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 391-0526

FAX: (212) 278-0400

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-555-268A-15

Query Match 10.8%; Score 71.5; DB 2; Length 384;
Best Local Similarity 25.9%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

QY 16 RQTLLINPRGVNPTN-----GVA-----SLSQAGAVPALEKRVTVSVSOPSRRNKRYKVQVK 67
DB 138 RHQLLINPRGWRPNRHHAYVGIWVLAIVASSLPFLIYQ--VMTDEPRQN----- 186
QY 68 IONPACTANGSCDPSVTRQKADVTFSFTQYSTDEBRAPVTELAAL 115
DB 187 -----VTLDAYKDKYVCFDQPPSDSHRLSYTTLTLVL 218

RESULT 8

US-09-200-673-15
Sequence 15, Application US/09200673A
Patent No. 6316203

GENERAL INFORMATION:

APPLICANT: Gerald, Christophe P.G.

APPLICANT: Weinshank, Richard L.

APPLICANT: Walker, Mary W.

APPLICANT: Branchek, Theresa

TITLE OF INVENTION: Methods of Modifying Feeding Behavior. Compounds Useful

TITLE OF INVENTION: in Such Methods, and DNA Encoding A Hypothalamic

FILE REFERENCE: 46166-BZ/JPW

CURRENT APPLICATION NUMBER: US/09/200,673A

EARLIER FILING DATE: 1998-11-25

EARLIER APPLICATION NUMBER: 08/566,096

EARLIER FILING DATE: 1995-12-01

EARLIER APPLICATION NUMBER: 08/349,025

EARLIER FILING DATE: 1994-12-02


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QY      16 RQTLLNPRGVNPVN-----GVA---SLSQAGVPALEKRYTVSVSQSRKRKKYKYQVK 67
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      141 RHQLIINPRGMRPNRRHAYGVIAVIWLAVASISLPIFYQ--VWTDEPFQN----- 189

QY      68 IQNPACTANGSCDPSYTRKRYADVTFESFOYSIDERARAVRTETAL 115
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      190 -----VTLDAYKDKYVCFDQFPDSHRLSYTTILLVL 221

RESULT 13
COM URGAT 112277 Z

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RESULT 13
PCT-US95-14377-3
; Sequence 3, Application PC/TUS9514377
; GENERAL INFORMATION:
; APPLICANT: STRADER, CATHERINE D.
; ADDRESS: 3000 WEST WASHINGTON A

TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
NUMBER OF SEQUENCES: 11
CONTACT/INVENTOR ADDRESS:

ADDRESSEE: MARY A. APPOLLINA
STREET: 126 EAST LINCOLN AVENUE
CITY: RAHWAY
COUNTY: UNION

```

; ZIP: 07065-0900
; COMPUTER READABLE FORM:
;

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.30
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;      ***** 1989-1990 Data *****

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APPLICATION NUMBER: PCT/US95/143777
FILING DATE:
CLASSIFICATION:
PRIORITY DATE:

APPLICATION NUMBER: US 08/335,011
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: ADDRESS: CITY: STATE: ZIP: COUNTRY: PHONE: FAX: E-MAIL: URL: COMMENTS: OTHER: SIGNATURE: DATE: TITLE: FIRM: ADDRESS: CITY: STATE: ZIP: COUNTRY: PHONE: FAX: E-MAIL: URL: COMMENTS: OTHER: SIGNATURE: DATE: TITLE: FIRM:

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;
;   REGISTRATION NUMBER: 34,087
;   REFERENCE/DOCKET NUMBER: 19339Y PCT
;   TELECOMMUNICATION INFORMATION:
;   ATTORNEY (0000) 504 3450

```

```

; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3
; SEQUENCE CHARACTERISTICS:
;

```

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;

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PCT-US95-14377-3	
Query Match	10

Matches	28; Conservative
QY	16 RQTLVLNPRGVNPT

Db 141 RHQLINPRGWRPNRRHAYGIAVIVLWLVASSLPLELYQ--VMTDEPFQN----- 189

RESULT 14
US-09-270-767-44620

RESULT 14
US-09-270-767-44620
; Sequence 44620, Application US/0927076-
; Patent No. 6703491

A:

189

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: GENERAL INFORMATION:
: APPLICANT: Homburger et al.
: TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
: FILE REFERENCE: File Reference: 7326-094
: CURRENT APPLICATION NUMBER: US/09/270.767
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ ID NOS: 62517
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 44620
: LENGTH: 502
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
: FEATURE:
: OTHER INFORMATION: Xaa means any amino acid
: US-09-270-767-44620

Query Match      10.6%; Score 70.5; DB 4; Length 502;
Best Local Similarity 24.2%; Pred.No. 6.6;
Matches 29; Conservative 20; Mismatches 52; Indels 19; Gaps 4,

QY      18 TLVNPGRVNTNGVSLSQGANPALEKRYTVSYSQP-----SRKRKYKQVQKQN 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      258 TIAVN---ISPSBPPTQPQIPEPEQVNSYTVVASPEVPPVAXARDRRKQTRSTIKN 314
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      71 PTACTANGSCPSPTVRQKADVTSTFQ-----YSTDERAPVRT--ETLAALLASPL 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      315 AXXYVKTFCSTSSATRHSTRICISSTVSSQLSPPLGKADKDFVKTILPATPTFSFNL 374
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-08-090-148-1
: Sequence 1, Application US/08090148
: Patent No. 5534257
: GENERAL INFORMATION:
: APPLICANT: Mastico, Robert Allan
: APPLICANT: Stockley, Peter George
: APPLICANT: Talbot, Simon John
: TITLE OF INVENTION: Antigen-presenting Capsid with
: TITLE OF INVENTION: Fusion MS2-Coat Protein
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Roseman & Colin
: STREET: 575 Madison Avenue
: CITY: New York
: STATE: NY
: COUNTRY: U.S.A.
: ZIP: 10022-2585
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5", 1.44MB
: COMPUTER: IBM PS2-486
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/090.148
: FILING DATE: 08/11/93
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9101550.3
: FILING DATE: 01/24/91
: APPLICATION NUMBER: PCT/GB92/00124
: FILING DATE: 01/22/92
: ATTORNEY/AGENT INFORMATION:
: NAME: Nissenbaum, Israel
: REGISTRATION NUMBER: 27,582
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 940-8636
: TELEFAX: (212) 940-6404
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 129 AMINO ACIDS
: TYPE: AMINO ACID
: TOPOLOGY: NOT RELEVANT

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:16:27 ; Search time 32.7351 Seconds
(without alignment)
1450.557 Million cell updates/sec

Title: US-10-622-064-10
Perfect score: 664
Sequence: 1 ARLEVTYLGNIKGDRQTLV.....AALIASPLIDAIQINPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgns2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgns2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgns2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgns2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgns2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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10: /cgns2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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15: /cgns2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	100.0	132	14	US-10-243-739-27
2	664	100.0	132	14	US-10-244-065-27
3	664	100.0	132	14	US-10-289-454-27
4	664	100.0	132	14	US-10-050-902-258
5	664	100.0	132	14	US-10-050-898-258
6	664	100.0	132	14	US-10-346-190-27
7	664	100.0	132	15	US-10-465-811-18
8	664	100.0	132	15	US-10-289-456-27
9	664	100.0	132	15	US-10-622-064-10
10	664	100.0	132	15	US-10-622-124-21
11	664	100.0	132	16	US-10-622-087-21
12	661	99.5	132	14	US-10-243-739-26
13	661	99.5	132	14	US-10-244-065-26

14	661	99.5	132	14	US-10-289-454-26	Sequence 26, App1
15	661	99.5	132	14	US-10-050-902-259	Sequence 259, App
16	661	99.5	132	14	US-10-050-898-259	Sequence 259, App
17	661	99.5	132	14	US-10-346-190-26	Sequence 26, App1
18	661	99.5	132	15	US-10-465-811-17	Sequence 17, App1
19	661	99.5	132	15	US-10-289-456-26	Sequence 26, App1
20	661	99.5	132	15	US-10-622-064-9	Sequence 9, App1
21	661	99.5	132	15	US-10-622-124-20	Sequence 20, App1
22	661	99.5	132	16	US-10-622-087-20	Sequence 20, App1
23	658	99.1	132	14	US-10-243-739-25	Sequence 25, App1
24	658	99.1	132	14	US-10-244-065-25	Sequence 25, App1
25	658	99.1	132	14	US-10-050-902-257	Sequence 257, App
26	658	99.1	132	14	US-10-050-898-257	Sequence 257, App
27	658	99.1	132	14	US-10-346-190-25	Sequence 25, App1
28	658	99.1	132	15	US-10-465-811-16	Sequence 16, App1
29	658	99.1	132	15	US-10-289-456-25	Sequence 25, App1
30	658	99.1	132	15	US-10-622-064-8	Sequence 8, App1
31	658	99.1	132	15	US-10-622-124-19	Sequence 19, App1
32	658	99.1	132	15	US-10-622-087-19	Sequence 19, App1
33	658	99.1	132	16	US-10-243-739-23	Sequence 23, App1
34	655	98.6	132	14	US-10-244-065-23	Sequence 23, App1
35	655	98.6	132	14	US-10-050-898-235	Sequence 235, App
36	655	98.6	132	14	US-10-050-902-255	Sequence 255, App
37	655	98.6	132	14	US-10-050-898-255	Sequence 255, App
38	655	98.6	132	14	US-10-346-190-23	Sequence 23, App1
39	655	98.6	132	15	US-10-465-811-14	Sequence 14, App1
40	655	98.6	132	15	US-10-289-456-23	Sequence 23, App1
41	655	98.6	132	15	US-10-622-064-6	Sequence 6, App1
42	655	98.6	132	15	US-10-622-124-17	Sequence 17, App1
43	655	98.6	132	16	US-10-622-087-17	Sequence 17, App1
44	655	98.6	132	16	US-10-243-739-10	Sequence 10, App1
45	652	98.2	132	14	US-10-243-739-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-10-243-739-27
Sequence 27, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Stornli, Tazio
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
FILE REFERENCE: 1700.0210001
CURRENT FILING DATE: 2002-09-16
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-27

Query Match	100.0%	Score 664	DB 14	Length 132
Best Local Similarity	100.0%	Pred. No. 1.6e-66		
Matches 132	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ARLEVTYLGNIKGDRQTLVLPNGVNPNGVYASLSQAGVPALEKRVTVSVSQSRNRK	60	
DB	1	ARLEVTYLGNIKGDRQTLVLPNGVNPNGVYASLSQAGVPALEKRVTVSVSQSRNRK	60	
QY	61	NYKVQVKIOMPACTANGSCDPSVTRKQADVTFSFTQYSTDEBRAPVTELAALIASPL	120	
DB	61	NYKVQVKIOMPACTANGSCDPSVTRKQADVTFSFTQYSTDEBRAPVTELAALIASPL	120	
QY	121	LIDAIQINPAY 132		

Db 121 LIDAIQOLNPAY 132

RESULT 2

US-10-244-065-27
Sequence 27, Application US/10244065
Publication No. US20030095668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tisot, Alain
APPLICANT: Schwarz, Katrin
APPLICANT: Meijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumps, Paul
APPLICANT: Cielens, Induls
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-Like Particles
FILE REFERENCE: 1700.022001
CURRENT APPLICATION NUMBER: US/10/244,065
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-27

Query Match 100.0%; Score 664; DB 14; Length 132;

Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRNRK 60
DB 1 ARLEVTTLGNIGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 3

US-10-289-454-27
Sequence 27, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.036001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-259
US-10-289-454-27

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRNRK 60
DB 1 ARLEVTTLGNIGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 4

US-10-050-902-258
Sequence 258, Application US/1005902
Publication No. US20030175290A1
GENERAL INFORMATION:
APPLICANT: Renner, Wolfgang A.
APPLICANT: Bachmann, Martin
APPLICANT: Tisot, Alain
APPLICANT: Maurer, Patrick
APPLICANT: Lechner, Franziska
APPLICANT: Seibel, Peter
APPLICANT: Piossek, Christine
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.019004
CURRENT APPLICATION NUMBER: US/10/050,902
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,379
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 258
LENGTH: 132
TYPE: PRT
ORGANISM: Qb 259
US-10-050-902-258

Query Match 100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRNRK 60
DB 1 ARLEVTTLGNIGKDGROTLVLPNGVPTNGVASLSQAGAVPALEKRVTVSVSOPSRNRK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

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RESULT 5
US-10-050-898-258
; Sequence 258, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tisoc, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Seibel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Orlmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050, 898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 258
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 259
US-10-050-898-258

Query Match      100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARLEVTYIGNIGKGRQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60
Db      1 ARLEVTYIGNIGKGRQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60

Qy      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTEIAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTEIAALLASPL 120

Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

RESULT 6
US-10-346-190-27
; Sequence 27, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pellicioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
```

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; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 27
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Qb 259
US-10-346-190-27

Query Match      100.0%; Score 664; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARLEVTYIGNIGKGRQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60
Db      1 ARLEVTYIGNIGKGRQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60

Qy      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTEIAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTEIAALLASPL 120

Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

RESULT 7
US-10-465-811-18
; Sequence 18, Application US/10465811
; Publication No. US2004000538A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 18
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
US-10-465-811-18

Query Match      100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARLEVTYIGNIGKGRQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60
Db      1 ARLEVTYIGNIGKGRQTLVLPNGVNPPTNGVASISQAGAVPALEKRYTVSVSOPSRNRK 60

Qy      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTEIAALLASPL 120
Db      61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTEIAALLASPL 120

Qy      121 LIDAIDQNPAY 132
Db      121 LIDAIDQNPAY 132

RESULT 8
US-10-289-456-27
; Sequence 27, Application US/10289456
```

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; Publication No. US2004003211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Mauret, Patrick
; APPLICANT: Spohn, Gunter
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.033001
; CURRENT APPLICATION NUMBER: US/10/289,456
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Q-beta 259 mutant
; US-10-289-456-27

```

Query Match	100.0%	Score 664	DB 15	Length 132
Best Local Similarity	100.0%	Pred. NO. 1.6e-66		
Matches 132	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ARLETVLLGNIGKGRQTLVLPGRVNPNTNGVASLSQAGAVPALEKRYTVSVQPSRRRK	60	
Db	1	ARLETVLLGNIGKGRQTLVLPGRVNPNTNGVASLSQAGAVPALEKRYTVSVQPSRRRK	60	
QY	61	NYKQVKIQNTACTANGSCDPSVTRQKKADVTFSFTQYSTDEERAFVRTLEAALLASPL	120	
Db	61	NYKQVKIQNTACTANGSCDPSVTRQKKADVTFSFTQYSTDEERAFVRTLEAALLASPL	120	
QY	121	LIDALDQLNPAY	132	
Db	121	LIDALDQLNPAY	132	

```

1      RESULT 9
2      US-10-622-064-10
3      ; Sequence 10, Application US/10622064
4      ; Publication No. US20040059094A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Bachmann, Martin F
7      ; APPLICANT: Maurer, Patrick F
8      ; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
9      ; FILE REFERENCE: 1700.0300001
10     ; CURRENT APPLICATION NUMBER: US/10/622,064
11     ; CURRENT FILING DATE: 2003-07-18
12     ; PRIOR APPLICATION NUMBER: US 60/396,575
13     ; PRIOR FILING DATE: 2002-07-18
14     ; NUMBER OF SEQ ID NOS: 33
15     ; SOFTWARE: PatentIn version 3.2
16     ; SEQ ID NO 10
17     ; LENGTH: 132
18     ; TYPE: PRT
19     ; ORGANISM: Artificial Sequence
20     ; FEATURE:
21     ; OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
22     ; US-10-622-064-10

```

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Query Match      100.0%; Score 664; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARLETVLLGNIGKGRQTLVLPNPRVNTNGVASISQAGVPALEKRTVSVSOPSRRRK 60
|||||

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Db	1	ARLEETLGNIGDGDGQTLVLPNPGVNPFTNGVASLSQAGVPALEKVTWSVSQSPSNRK	60
Qy	61	NYKVQVKI ONPRACTCTNGSCDPSVTRKXADVDYFSTGYSTDEERAFVRETELALLASPL	120
Db	61	NYKVQVKI QNPRACTCTNGSCDPSVTRKXADVDYFSTGYSTDEERAFVRETELALLASPL	120
Qy	121	LIDAIQDLNPAY	132
Db	121	LIDAIQDLNPAY	132

```

RESULT 10
US-10-622-124-21
; Sequence 21, Application US/10622124
; Publication No. US20040076645A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Falturija, Alma
; TITLE OF INVENTION: Ghrelin-Carrier Conjugates
; FILE REFERENCE: 1700.0340001
; CURRENT APPLICATION NUMBER: US/10/622,124
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,638
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ. ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 132
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
; US-10-622-124-21

```

Query March	100.0%;	Score 664;	DB 15;	Length 132;
Best Local Similarity	100.0%;	Pred. No. 1.6e-66;		
Matches 133;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ARLETVTLGNIGKDGQRLVILNPRGVNPTNGVASISQAGVPALEKRYTVSVSQPSNRK	60	
Db	1	ARLETVTLGNIGKDGQRLVILNPRGVNPTNGVASISQAGVPALEKRYTVSVSQPSNRK	60	
QY	61	NYKYQKIQNPACTANGSCDPSVTRQKADVTBSFTQYSTDERRAFRIETLALLSPL	120	
Db	61	NYKYQKIQNPACTANGSCDPSVTRQKADVTBSFTQYSTDERRAFRIETLALLSPL	120	
QY	121	LIDAIIDQLNPAY	132	
Db	121	LIDAIIDQLNPAY	132	

```

; RESULT 11
; US-10-622-087-21
; Sequence 21, Application US/10622087
; Publication No. US20040141984A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tisot, Alain
; APPLICANT: Ottmann, Rainer
; APPLICANT: Imond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
; FILE REFERENCE: 1700.0350002
; CURRENT APPLICATION NUMBER: US/10/622,087
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,639
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/470,432
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21

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LENGTH: 132
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Bacteriophage Q-beta 259 mutant
US-10-622-087-21

Query Match 100.0%; Score 664; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-66;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNK 60
DB 1 ARLEVTLTGNIGKDGKQRLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQNLMPAY 132
DB 121 LIDAIDQNLMPAY 132

RESULT 12
US-10-243-739-26
Sequence 26, Application US/10243739
Publication No. US20030091593A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
FILE REFERENCE: 1700.0210001
CURRENT APPLICATION NUMBER: US/10/243,739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/318,967
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-243-739-26

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNK 60
DB 1 ARLEVTLTGNIGKDGKQRLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQNLMPAY 132
DB 121 LIDAIDQNLMPAY 132

RESULT 13
US-10-244-065-26
Sequence 26, Application US/10244065
Publication No. US20030099668A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin F.
APPLICANT: Storni, Tazio
APPLICANT: Maurer, Patrick
APPLICANT: Tissot, Alain

APPLICANT: Schwarz, Katrin
APPLICANT: Weijerink, Edwin
APPLICANT: Lipowsky, Gerard
APPLICANT: Pumpens, Paul
APPLICANT: Cielens, Indulis
APPLICANT: Renhofa, Regina
TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particle
TITLE OF INVENTION: Method of Preparation and Use
FILE REFERENCE: 1700.0220001
CURRENT APPLICATION NUMBER: US/10/244,065
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/374,145
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/318,994
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta
US-10-244-065-26

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNK 60
DB 1 ARLEVTLTGNIGKDGKQRLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNK 60
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
DB 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEBERAFVTELAALLASPL 120
QY 121 LIDAIDQNLMPAY 132
DB 121 LIDAIDQNLMPAY 132

RESULT 14
US-10-289-454-26
Sequence 26, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Jennings, Gary
APPLICANT: Sonderegger, Ivo
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 132
TYPE: PRT
ORGANISM: Bacteriophage Q-beta-251
US-10-289-454-26

Query Match 99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLEVTLTGNIGKDGKQRLVLPNGVNPPTNGVASLSQAGAVPALERKRVTVSVSOPSRNK 60

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Db      1  AKLETTVLGNIGKDGROTLVLPNGVNPINGVASLSQAGAVPALERKVTVSQPSRNRK 60
QY      61  NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
Db      61  NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
QY      121  LIDAIQOLNPAY 132
Db      121  LIDAIQOLNPAY 132
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RESULT 15

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US-10-050-902-259
/ Sequence 259, Application US/10050902
/ Publication No. US20030175290A1
/ GENERAL INFORMATION:
/ APPLICANT: Renner, Wolfgang A.
/ APPLICANT: Bachmann, Martin
/ APPLICANT: Tisbet, Alain
/ APPLICANT: Maurer, Patrick
/ APPLICANT: Lechner, Franziska
/ APPLICANT: Seibel, Peter
/ APPLICANT: Piossek, Christine
/ TITLE OF INVENTION: Molecular Antigen Array
/ FILE REFERENCE: 1700.0190004
/ CURRENT APPLICATION NUMBER: US/10/050,902
/ CURRENT FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/262,379
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: US 60/288,549
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/326,998
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: US 60/331,045
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 350
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 259
/ LENGTH: 132
/ TYPE: PRT
/ ORGANISM: Qb 251
US-10-050-902-259
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Query Match      99.5%; Score 661; DB 14; Length 132;
Best Local Similarity 99.2%; Pred. No. 3.5e-66;
Matches 131; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1  ARLETTVLGNIGKDGROTLVLPNGVNPINGVASLSQAGAVPALERKVTVSQPSRNRK 60
Db      1  AKLETTVLGNIGKDGROTLVLPNGVNPINGVASLSQAGAVPALERKVTVSQPSRNRK 60
QY      61  NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
Db      61  NYKVQVKIQNPACTANGSCDPSVTROKXADVTFSFTQYSTDERAFVTEIAALLASPL 120
QY      121  LIDAIQOLNPAY 132
Db      121  LIDAIQOLNPAY 132
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Search completed: January 4, 2005, 09:41:23
Job time : 32.7351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:51 ; Search time 7.8938 Seconds
(without alignments)
1609.836 Million cell updates/sec

Title: US-10-622-064-10
Perfect score: 664
Sequence: 1 ARLEVTVLGNIGKDGRTLV.....ALLASPLLDALDQNPAY 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652	98.2	132	1	VCBPOB coat protein - pha
2	528.5	79.6	331	1	S01964 readthrough protei
3	116	17.5	131	1	VCBPR1 coat protein - pha
4	89.5	13.5	530	2	S22340 seeligeriolysin -
5	85.5	12.9	540	2	T00646 hypotethical prote
6	84.5	12.7	529	2	S24231 listeriolysin prec
7	84.5	12.7	529	2	A43505 listeriolysin O pr
8	84.5	12.7	529	2	AC1100 listeriolysin O pr
9	80.5	12.1	528	2	S22341 ivanolysin precurs
10	80.5	12.1	1502	1	RGBYH1 CYP1/CYP3 transcript
11	79	11.9	282	2	A10186 probable iron-side
12	79	11.9	432	2	T31660 hypotethical prote
13	78.5	11.8	1861	2	T13845 microtubule-associ
14	78	11.7	830	2	S57537 MKT1 protein - yea
15	76.5	11.5	136	2	C38221 hypotethical prote
16	76.5	11.5	136	2	AS3065 conserved hypoteth
17	76.5	11.5	1052	2	C64221 hypotethical 114k
18	75.5	11.4	1097	2	AD2572 hypotethical prote
19	75	11.3	130	1	A46324 coat protein - pha
20	75	11.3	130	1	VCBPR3 coat protein - pha
21	74.5	11.2	130	1	VCBPR4 coat protein - pha
22	74.5	11.2	130	1	VCBPR5 coat protein - pha
23	74	11.1	340	2	S18650 homeotic protein H
24	74	11.1	340	2	A42008 homeotic protein H
25	73.5	11.1	191	2	H90078 hypotethical prote
26	73.5	11.1	520	1	ACMSD1 nicotinic acetylch
27	73.5	11.1	601	2	ACMSD1 serine/threonine k
28	73.5	11.1	719	2	T39271 conserved hypoteth
29	73	11.0	430	2	G88884 protein K09B11.10

30	72.5	10.9	129	1	VCBPR2 coat protein - pha
31	72.5	10.9	129	1	VCBPR7 coat protein - pha
32	72.5	10.9	129	1	VCBPR8 coat protein - pha
33	72	10.8	376	2	C84316 hypotethical prote
34	71.5	10.8	384	2	A45490 neuropeptide Y/pep
35	71	10.7	248	2	A86786 conserved hypoteth
36	71	10.7	399	1	A43685 polymerase-associ
37	71	10.7	463	2	S00676 translation elonga
38	71	10.7	1461	2	B90696 hypotethical prote
39	71	10.7	1461	2	A85547 hypotethical prote
40	71	10.7	1545	2	T42751 sulfonyleurea recep
41	71	10.7	1545	2	T46645 conserved hypoteth
42	70.5	10.6	836	2	A13237 sulfonyleurea recep
43	70	10.5	243	1	VHVUP1 nucleocapsid prote
44	70	10.5	425	2	S69796 pectate lyase (BC
45	69.5	10.5	130	1	VCBPM2 coat protein [vali

ALIGNMENTS

RESULT 1
VCBPOB
coat protein - phage Q-beta
C:Species: phage Q-beta
C:Date: 29-Jul-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004
C:Accession: A92240; A92221; A92088; A04224
R:Escarims, C.; Sastry, P.A.; Billeter, M.A.
J: Biol. Chem. 253, 8390-8399, 1978
A:Title: Determination of the first half of the coat protein cistron of bacteriophage Qb
A:Reference number: A92240; MUID:79048469; PMID:361741
A:Accession: A92240
A:Molecule type: mRNA
A:Residues: 1-80 <ESG>
A:Cross-references: UNIPROT:P03615
R:Stoll, E.; Wilson, K.J.; Reiser, J.; Weissmann, C.
J: Biol. Chem. 252, 990-993, 1977
A:Title: Revised amino acid sequence of Qbeta coat protein between positions 1 and 60.
A:Reference number: A92221; MUID:77118576; PMID:838709
A:Accession: A92221
A:Molecule type: protein
A:Residues: 1-60 <STO>
R:Malta, T.; Konigsberg, W.
J: Biol. Chem. 246, 5003-5024, 1971
A:Title: The amino acid sequence of the Qbeta coat protein.
A:Reference number: A92088; MUID:71288580; PMID:5570434
A:Accession: A92088
A:Molecule type: protein
A:Residues: 1-21, 'D', '23-55, 57-132 <MAI>
C:Superfamily: phage GA coat protein

Query Match 98.2% Score 652; DB 1; Length 132;
Best Local Similarity 97.7% Pred. No. 1.6e-56;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	ARLEVTVLGNIGKDGRTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSPSRNRK	60
DB	1	AKLEVTVLGNIGKDGRTLVNPRGVNPTNGVASISQAGAVPALEKRTVSVSPSRNRK	60
QY	61	NYKVQVKIQNPACTANGSCDPSVTRQKADVTGFTQYSTDEERAFTREIAALLASPL	120
DB	61	NYKVQVKIQNPACTANGSCDPSVTRQKADVTGFTQYSTDEERAFTREIAALLASPL	120
QY	121	LIDALDQNPAY 132	
DB	121	LIDALDQNPAY 132	

RESULT 2
S01964
readthrough protein - phage SP
C:Species: phage SP
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:/Accession: S01964
C:/Inokuchi, Y.; Jacobson, A.B.; Hirose, T.; Inayama, S.; Hirashina, A.
Nucleic Acids Res. 16, 6205-6221, 1988
A:/Title: Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP.
A:/Reference number: S01963; MUID:88289362; PMID:339390
A:/Accession: S01964
A:/Status: Preliminary
A:/Molecule type: genomic RNA
A:/Residues: 1-331 <INO>
A:/Cross-references: UNIPROT:P09677; EMBL:X07489
C:/Superfamily: phage GA coat protein

Query Match
Best Local Similarity 79.6%; Score 528.5; DB 2; Length 331;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 ARLEVTLTGNTGKDGROTLVLPNGVNPTNGVASLSQAGVPALKEKYTVSVSOPSRNRK 60
Db 2 AKLNQVTLSTKGKNDQTLLTPRGVNPTNGVASLSQAGVPALKEKYTVSVSOPSRNRK 61
QY 61 NYKKQVKIQNPACTANGSCDPSVTRKQADVTFSFTQYSTDEERAFVRETAALLASPLI 120
Db 62 NFKQIKIQNPACTCRD-ACDPSTRSAPADVTLISFYSIDBERALIRTELALLADPL 120
QY 121 LIDAIDLNPAY 132
Db 121 IVDAILDLNPAY 132

RESULT 3
VCBPPI
coat protein - phage PRRI
C:/Species: Phage PRRI
C:/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C:/Accession: A04225
R:/Daese, P.; Vandekerckhove, J.S.; Van Montagu, M.C.
Eur. J. Biochem. 94, 375-386, 1979
A:/Title: The primary structure of the coat protein of the broad-host-range RNA bacteriophage phi-X174
A:/Reference number: A04225; MUID:79148387; PMID:107028
A:/Molecule type: Protein
A:/Residues: 1-131 <DNH>
A:/Cross-references: UNIPROT:P03616
C:/Superfamily: phage GA coat protein

Query Match
Best Local Similarity 17.5%; Score 116; DB 1; Length 131;
Matches 42; Conservative 14; Mismatches 50; Indels 16; Gaps 5;

QY 17 QTVLNLGRGNPT-----NGVASLSQAGVPALKEKYTVSVSOPSRNRKRYKQV 66
Db 4 QNVLPKREATPNDHTFPVRDIRDNVGGEVSTGVPIGESFFTSLRRTSNGR--YKSTL 61
QY 67 KIQNPT--ACTANGSCDPSVTRKQADVTFSFTQYSTDEER-AFVRETAALLASPLI- 122
Db 62 KLVVPPVQSQVINGVTPVVVRTSYTYDFDYDAARSTTKERNNFVGMIALDKADMIVH 121
QY 123 DAIDLNPAY 132
Db 122 DTIVNLQGVY 131

RESULT 4
S22340
seeligeriolysin - Listeria seeligeri
C:/Species: Listeria seeligeri
C:/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:/Accession: S22340
R:/Haas, A.; Dumbeky, M.; Kreft, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A:/Title: Listeriolysin genes: complete sequence of ilo from Listeria ivanovi and of lsc

A:Accession: S22340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <HAA>
A:Cross-references: UNIPROT:P31830; EMBL:X60462; NID:g44144; PIDN:CAA42996.1; PID:g44145
A:Note: the authors translated the codon GCC for residue 287 as Pro
C:superfamily: dipeptide transport protein

Query Match 13.5%; Score 89.5; DB 2; Length 530;
Best Local Similarity 25.0%; Pred. No. 0.71; Mismatches 37; Indels 43; Gaps 7;
Matches 34; Conservative 22;

Qy 13 KDGQTLVL-NPRGVNPT-----NGVASLSQAGA-----VPALEKRV 48
Db 94 KDGSYIVVEKKKKKGINNNADISVINAISLTYPGALVYKANELVENQPVLPVKRDSL 153
Qy 49 TVSVQPSNRKNRYKQVQKIONPTACTANGSCDPSVTR-QKY-----ADYTFSTQ 98
Db 154 TLISVLPFGMTTKDKNKIFVK-NPTKSNVNVAVTLVERMNDKYSKAVPNINAKIDYS--- 208
Qy 99 YSTDERAPVFTLEAA 114
Db 209 ----DEMAYSESQLIA 220

RESULT 5
T00646
hypothetical protein F316.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00646
R:Federalbio, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo,
R.; Vysotskaya, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z14197
A:Accession: T00646
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-540 <FED>
A:Cross-references: UNIPROT:Q48683; EMBL:AC002396; NID:g2749918; PIDN:AAC00577.1; PID:g22
C:Genetics:
A:Gene: ATSP:F316.9
A:Map position: 1
A:Introns: 14/3; 428/3; 448/2; 483/3; 502/3
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-binding

Query Match 12.9%; Score 85.5; DB 2; Length 540;
Best Local Similarity 26.1%; Pred. No. 1.8; Mismatches 55; Indels 15; Gaps 3;
Matches 30; Conservative 15;

Qy 11 IGDGRQTLVLNPRG---VNPTNGVASLSQAGAVPALERKRYTVSVQPSNRKN-YKQV 66
Db 255 VKKEKKPNILIKKNDGNVRINPTRGLKPNQVGKPEINTKVTISRKTPSPKEMKMKATK 314
Qy 67 KIONPTACTANGSCDPSVTRKYADYTFSTQYSTDEERAPVFTLEAAIASPLL 121
Db 315 KPAPMSPGSGFAPRKYKAPATKTSLSHSLKKEK-----VSPILL 358

RESULT 6
S24231
listeriolysin precursor - Listeria monocytogenes (strain 12067)
C:Species: Listeria monocytogenes
A:Variety: strain 12067
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S24231
R:Raumussen, O.F.; Beck, T.; Olsen, J.E.; Dons, L.; Rossen, L.
Infect. Immun. 59, 3945-3951, 1991
A:Title: Listeria monocytogenes isolates can be classified into two major types according
A:Reference number: S24230; MUID:92040062; PMID:1937753
A:Accession: S24231
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-529 <RAS>
A:Cross-references: UNIPROT:P13128; EMBL:X60035; NID:g44110; PIDN:CAA42639.1; PID:g44112
A:Experimental source: strain 12067, serotype 4b
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C:Genetics:
A:Gene: hlyA
C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-529/Product: listeriolysin O #status predicted <MAT>
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KDGRQTLVL-----NPRGVNPTNGVASISQAGA-----VPALKKRV 48
DB 93 KDGRNYIYVEKKKKSINQNNADIQVNNAISSLITFGALVKANSELVENQPDVLPVKRDSL 152
QY 49 TVSVSQPSRRNRKRYQVQKIQNPACTANGSCDPSVTR-----QKYADVTFSTFOYSTD 102
DB 153 TLTSLDLPGMTNQDNKIYVK--NATKSNVNNNAVNTLVERNKKYQAQYPRVS---AKIDYD 207
QY 103 EERAFVRTFLA 114
DB 208 DEMAYSESQLIA 219
RESULT 7
A43505
Listeriolysin O precursor - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 21-Oct-1992 #sequence revision 21-Oct-1992 #text_change 09-Jul-2004
C:Accession: A43505; S05306; A47606; S12400; A61079
R:Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanrey
Infect. Immun. 56, 766-772, 1988
A:Title: Expression in Escherichia coli and sequence analysis of the listeriolysin O det
A:Reference number: A43505; MUID:88153053; PMID:3126142
A:Accession: A43505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <MEN>
A:Cross-references: UNIPROT:P13128; GB:M24199; NID:g149652; PIDN:AA03018.1; PID:g149653
A:Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R:Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A:Title: Nucleotide sequence of the listeriolysin gene from a Listeria monocytogenes ser
A:Reference number: S05306; MUID:89366684; PMID:2505236
A:Accession: S05306
A:Molecule type: DNA
A:Residues: 1-529 <DOM>
A:Cross-references: EMBL:X15127; NID:g44106; PIDN:CAA33223.1; PID:g44107
A:Experimental source: strain EGD from a weakly hemolytic strain, serotype 1/2a
A:Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R:Mengaud, J.; Chenevert, J.; Geoffroy, C.; Gaillard, J.L.; Cosset, P.
Infect. Immun. 55, 3225-3227, 1987
A:Title: Identification of the structural gene encoding the SH-activated hemolysin of Li
A:Reference number: A47606; MUID:88057627; PMID:2824384
A:Accession: A47606
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 413-480 <ME2>
A:Cross-references: GB:M29171
R:Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cosset, P.
Mol. Microbiol. 4, 2167-2178, 1990
A:Title: Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtain
A:Accession: S12400; MUID:91211627; PMID:1965218
A:Reference number: S12400
A:Molecule type: DNA
A:Residues: 483-493 <MC>
A:Experimental source: strain L028, serotype 1/2c
C:Genetics:
A:Gene: hlyA, hlyA, hlyA

C:Superfamily: dipeptide transport protein
C:Keywords: virulence factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-529/Product: listeriolysin O #status predicted <MAT>
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KDGRQTLVL-----NPRGVNPTNGVASISQAGA-----VPALKKRV 48
DB 93 KDGRNYIYVEKKKKSINQNNADIQVNNAISSLITFGALVKANSELVENQPDVLPVKRDSL 152
QY 49 TVSVSQPSRRNRKRYQVQKIQNPACTANGSCDPSVTR-----QKYADVTFSTFOYSTD 102
DB 153 TLTSLDLPGMTNQDNKIYVK--NATKSNVNNNAVNTLVERNKKYQAQYPRVS---AKIDYD 207
QY 103 EERAFVRTFLA 114
DB 208 DEMAYSESQLIA 219
RESULT 8
AC1100
Listeriolysin O precursor [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1100
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feiki, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapatk, G.; Madueno, E.; Maltournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Botand, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <GLA>
A:Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:g16409567; GSPDB:C
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: hly
C:Superfamily: dipeptide transport protein
Query Match 12.7%; Score 84.5; DB 2; Length 529;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 30; Conservative 23; Mismatches 44; Indels 35; Gaps 5;
QY 13 KDGRQTLVL-----NPRGVNPTNGVASISQAGA-----VPALKKRV 48
DB 93 KDGRNYIYVEKKKKSINQNNADIQVNNAISSLITFGALVKANSELVENQPDVLPVKRDSL 152
QY 49 TVSVSQPSRRNRKRYQVQKIQNPACTANGSCDPSVTR-----QKYADVTFSTFOYSTD 102
DB 153 TLTSLDLPGMTNQDNKIYVK--NATKSNVNNNAVNTLVERNKKYQAQYPRVS---AKIDYD 207
QY 103 EERAFVRTFLA 114
DB 208 DEMAYSESQLIA 219
RESULT 9
S22341
Ivanolysin precursor - Listeria ivanovii
C:Species: Listeria ivanovii
C:Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S22341; S36683
R:Haas, A.; Dumbeky, M.; Kretz, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A:Title: Listeriolysin genes: complete sequence of llo from Listeria ivanovii and of lso
A:Reference number: S22340; MUID:92182018; PMID:1543752


```

A:Reference number: Z21049
A:Accession: T13650
A>Status: preliminary; translated from GB/EMBL/DDB
A:Molecule type: DNA
A:Residues: 1-432 <BIR>
A:Cross-references: UNIPROT:P91584; EMBL:Z83760; NID:e1014349; PID:e289996; PIDN:CA80605
C:Genetics:
A:Introns: 180/2; 212/1; 229/3

Query Match      11.9%; Score 79; DB 2; Length 432;
Best Local Similarity 28.3%; Pred.No. 5.9;
Matches 32; Conservative 16; Mismatches 47; Indels 18; Gaps 6;

QY      4  ETVLGNIGKGRQTLVTPNGVNPPTNGVALSQAQNPALAEKVTVSVSPSNRRKKY 63
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     242 DTSSEGETKGPGNLANP---TPSNARELGESVLETTVVSAIQ-EODSSAYR 297

QY      64 VQVIQNPTAC-TANGSC-----DPSVTROKAD-----VFPSFTQYSTDE 103
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     298 KE-NPQNAAPCPNRNGNCVSTNSKTPNDSKIETIVSDSDNTTDDTDIQTIDINE 349

RESULT 13
T13845
microtubule-associated protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A:Accession: T13845
J:Saunders, R.D.; Aviles, M.C.; Howard, T.; Gonzalez, C.; Glover, D.M.
J: Cell Biol. 137, 881-890, 1997
A>Title: The Drosophila gene abnormal spindle encodes a microtubule-associated protein t
A:Reference number: Z17792; MUID:97296495; PMID:9151690
A:Accession: T13845
A>Status: preliminary; translated from GB/EMBL/DDB
A:Molecule type: mRNA
A:Residues: 1-1861 <SAU>
A:Cross-references: UNIPROT:O01401; EMBL:U95171; NID:g1930121; PID:g1930122; PIDN:AAB515
C:Genetics:
A:Gene: asp
A:Cross-references: FlyBase:FBgn0000140
C:Function:
A>Description: is required for the normal function of the mitotic spindle

Query Match      11.8%; Score 78.5; DB 2; Length 1861;
Best Local Similarity 26.2%; Pred.No. 36;
Matches 38; Conservative 17; Mismatches 59; Indels 31; Gaps 5;

QY      2  RLEVTLTGNIKDKGRQLTVLPNGVNPPTNGVALSQAQ-----VP 42
          ||| | : : : : : : : : : : : : : : : : : : : : : :
DB     414 RNETHVAISPPKQRVEDTTL-PRSAAPNASARSSSAHAWPHAQSKPKLAQTWSLMKKP 472

QY      43 ALEKRVTVSVSPSNRRKNRYKVQVKIQ---NPACTANGSCDPSTEQKYADVTFPSFTQY 99
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     473 ATPKKVRRTSIQPS--VLYDSELYMQCINPDPEAAATTITIDPLASTMYID-----EQ 524

QY      100 STDERAFVRTSLALLASPLLIDA 124
          : : : : : : : : : : : : : : : : : : : : : :
DB     525 AVDRHQADFKKWLNATVISPADLDA 549

RESULT 14
S57537
MKII protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N2302; protein YND085w
C:Species: Saccharomyces cerevisiae
C>Date: 10-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
A:Accession: S57537; S50279; S63024; S63017; S65096
R:Solier-Mitz, A.; Salz, J.E.; Ballestra, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57533
A:Accession: S57537
A:Molecule type: DNA
A:Residues: 1-830 <SOI>
```

A:Cross-references: UNIPROT:P40850; EMBL:X89016; NID:g887621; PID:g887626
 R:Vertm. M.; Widner, W.R.; Dimman, J.D.; Wichter, R.B.
 A:Title: Sequence of MKT1, Nucleotide sequence of the L-A virus
 A:Reference number: S50279; NUID:95176705; PMID:7532890
 A:Accession: S50279
 A:Molecule type: DNA
 A:Residues: 1-29, 'G', '31-808, 'TMKTCNTVH' <VER>
 A:Cross-references: EMBL:U09129; NID:g520475; PID:AA049470.1; PID:g520476
 R:Solier-Mira, A.; Saiz, J.R.; Ballesta, J.P.G.; Remacha, M.
 A:Submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63018
 A:Accession: S63024
 A:Molecule type: DNA
 A:Residues: 1-830 <SON>
 A:Cross-references: EMBL:J71361; NID:g1301982; PID:g1301983; MIPS:YNL085W
 A:Experimental source: strain S288C
 R:Poehlmann, R.; Philippesen, P.
 A:Submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62997
 A:Accession: S63017
 A:Molecule type: DNA
 A:Residues: 569-830 <POE>
 A:Cross-references: EMBL:J71361; MIPS:YNL085W
 A:Experimental source: strain S288C
 R:Solier-Mira, A.; Saiz, J.R.; Ballesta, J.P.G.; Remacha, M.
 A:Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
 A:Reference number: S65092; NUID:96310628; PMID:8740422
 A:Accession: S65096
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-830 <SOF>
 A:Cross-references: EMBL:X89016; NID:g887621; PID:CAA61425.1; PID:g887626
 C:Genetics:
 A:Gene: SGD:MKT1
 A:Cross-references: SGD:S0005029; MIPS:YNL085W
 A:Map position: 14L
 C:Superfamily: Saccharomyces cerevisiae MKT1 protein
 C:Keywords: transmembrane protein
 P:615-631/Domain: transmembrane #status predicted <TMM>
 Query Match 11.7%; Score 78; DB 2; Length 830;
 Best Local Similarity 24.8%; Pred. No. 16;
 Matches 25; Conservative 21; Mismatches 49; Indels 6; Gaps 3;
 QY 5 TTTTGNIGDGGQTVLNRGVNPTNGVASLSGAGVPALEKRTVSVSOPSRKRYKV 64
 DB 301 STTLN---DSKENIQNYRGKISALRYMVLKDTGKVELFVGELIVSEDSKKNKDGK- 356
 QY 65 QVKIQNPACTANGSCDPSVTRQKADVTTFSPQVSTDEER 105
 DB 357 KSNLSSPS-SASSASAPATVTVTKANSEKLTVEKSTKEVR 395
 RESULT 15
 C98221
 Hypoetical protein AGR_L1428 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 09-Jul-2004
 C:Accession: C98221
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; NUID:21608551; PMID:11743194
 A:Accession: C98221
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <KUR>
 A:Cross-references: UNIPROT:Q8U873; GB:AE007870; PID:AAK69293.1; PID:g15159127; GSPDB:GR
 C:Genetics:
 A:Gene: AGR_L_1428

A;Map position: linear chromosome

Query Match	11.5%	Score 76.5;	DB 2;	Length 136;
Best Local Similarity	24.6%;	Pred. No. 2.7;		
Matches 29; Conservative	16;	Mismatches 56;	Indels 17;	Gaps 3;

[illegible]

Search completed: January 4, 2005, 09:17:32
Job time : 9.03224 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2005, 09:02:16 ; Search time 36.2676 Seconds
(without alignments)
2094.140 Million cell updates/sec

Title: US-10-622-064-10
Perfect score: 664
Sequence: 1 ARLEVTWLTGNIGKDGKQTLV.....AALLASPLLDALDQNLNPAV 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181.seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*\n1: uniprot_sprot:*\n2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652	98.2	132	1	COAT_BPOBE
2	652	98.2	133	2	AAM33126
3	652	98.2	132	2	Q8LTH1
4	652	98.2	132	2	AAL16663
5	563	84.8	133	2	Q9TOR9
6	563	84.8	133	2	Q64307
7	543	81.8	133	2	Q9TOS0
8	543	81.8	132	2	Q64303
9	528.5	79.6	132	1	COAT_BPSP
10	528.5	79.6	131	1	VAL_BPSP
11	496.5	74.8	132	2	Q9TOR8
12	496.5	74.8	131	2	Q64310
13	116	17.5	131	1	COAT_BPPRR
14	96.5	14.5	473	1	Q8VDC2
15	89.5	13.5	530	1	TACY_LISSE
16	89.5	13.5	530	2	AAR97361
17	85.5	12.9	540	2	Q48683
18	84.5	12.7	529	1	TACY_LISMP
19	84.5	12.7	529	1	TACY_LISMO
20	84.5	12.7	529	2	Q9LSB9
21	84.5	12.7	529	2	Q6R942
22	84.5	12.7	529	2	Q6R942
23	84.5	12.7	529	2	Q6R942
24	84.5	12.7	529	2	Q6R942
25	84.5	12.7	529	2	Q6R942
26	84.5	12.7	529	2	Q6R942
27	84.5	12.7	529	2	Q6R942
28	84.5	12.7	529	2	Q6R942
29	84.5	12.7	529	2	Q6R942
30	84.5	12.7	529	2	Q6R942
31	84.5	12.7	529	2	AAT03000

32	82	12.3	1624	2	Q9V3K8	Q9V3K8 drosophila
33	82	12.3	1637	2	Q9SRU8	Q9SRU8 drosophila
34	81	12.2	336	2	Q8TRF3	Q8TRF3 mechanosarc
35	80.5	12.1	528	1	TACY_LISIV	P31831 listeria iv
36	80.5	12.1	528	2	Q6R6D9	Q6R6D9 listeria iv
37	80.5	12.1	528	2	AAR97343	AAR97343 listeria
38	80.5	12.1	1502	1	CYP1_YEAST	P12351 saccharomyc
39	79	11.9	282	2	Q8ZF20	Q8ZF20 yersinia pe
40	79	11.9	282	2	AA61663	AA61663 yersinia
41	79	11.9	432	2	P91584	P91584 citra intes
42	79	11.9	512	2	Q6RGA7	Q6RGA7 bacillus th
43	78.5	11.8	525	2	Q6R6D0	Q6R6D0 listeria iv
44	78.5	11.8	525	2	AAR97352	AAR97352 listeria
45	78.5	11.8	1954	1	ASP_DROME	Q9VC45 drosophila

ALIGNMENTS

RESULT 1
COAT_BPOBE STANDARD; PRT; 132 AA.
ID COAT_BPOBE
AC P03615
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Alivolevirales.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Chelens I., Dreilima D., Dislers A., Baumann V.,
Ose V., Pumpens P.;
RT "Recombinant RNA phage Q-beta capsid particles synthesized and self-
assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
RN [2]
RP SEQUENCE OF 1-80 FROM N.A.
RX MEDLINE=79048469; PubMed=361741;
RA Escarmona C., Sastre P.A., Billeter M.A.;
RT "Determination of the first half of the coat protein cistron of
bacteriophage Q-beta as an application of a mapping procedure for RNA
fragments.";
RL J. Biol. Chem. 253:8390-8399(1978).
RN [3]
RP REVISIONS TO 1-60.
RX MEDLINE=77118576; PubMed=838709;
RA Stoll E., Wilson K.J., Reiser J., Weissmann C.;
RT "Revised amino acid sequence of Qbeta coat protein between positions 1
and 60.";
RL J. Biol. Chem. 252:990-993(1977).
RN [4]
RP SEQUENCE.
RX MEDLINE=71288580; PubMed=5570434;
RA Maite T., Konigsberg W.;
RT "The amino acid sequence of the Q-beta coat protein.";
RL J. Biol. Chem. 246:5003-5024(1971).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=96347354; PubMed=8736553;
RA Golmohammadi R., Fridborg K., Bunde M., Valgard K., Liljas L.;
RT "The crystal structure of bacteriophage Q-beta at 3.5-A resolution.";
RL Structure 4:543-554(1996).
CC -!- FUNCTION: Forms the phage shell; binds to the phage RNA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC
CC
DR EMBL; M99039; AAA16662.1; -;
DR EMBL; V00643; CAA23992.1; -;
DR PIR; A92240; VCBPOB.
DR PDB; IOBE; X-ray; A/B/C=1-132.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat; 1.
KW 3D-structure; Coat protein; Direct protein sequencing; RNA-binding.
FT INIT MET 0 0
FT CONFLICT 22 22 N -> D (in Ref. 4).
FT CONFLICT 56 56 Missing (in Ref. 4).
FT STRAND 6 9
FT TURN 13 14
FT STRAND 18 27
FT TURN 28 31
FT STRAND 32 36
FT HELIX 42 44
FT STRAND 47 53
FT STRAND 56 56
FT TURN 57 58
FT STRAND 59 59
FT STRAND 62 74
FT STRAND 83 96
FT TURN 98 99
FT HELIX 102 117
FT HELIX 119 126
FT TURN 127 127
SQ SEQUENCE 132 AA; 14123 MW; 1B7938C91CA5572E CRC64;

Query Match 98.2%; Score 652; DB 1; Length 132;
Best Local Similarity 97.7%; Pred. No. 3.4e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRRNK 60
DB 1 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRRNK 60
QY 61 NKVVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASPL 120
DB 61 NKVVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASPL 120
QY 121 LIDAIQOLNPAY 132
DB 121 LIDAIQOLNPAY 132

RESULT 2
AAM33126 PRELIMINARY; PRT; 133 AA.
ID AAM33126;
AC 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Coat protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolevivirus; Allolevivirus subgroup III.
OX NCBI_Taxid=12009;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
DR EMBL; AY099114; AAM33126.1; -;
KW Coat protein.
SQ SEQUENCE 133 AA; 14254 MW; 1B7967F0256C31DE CRC64;

Query Match 98.2%; Score 652; DB 2; Length 133;
Best Local Similarity 97.7%; Pred. No. 3.4e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRRNK 60
DB 2 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRRNK 61
QY 61 NKVVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NKVVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIQOLNPAY 132
DB 122 LIDAIQOLNPAY 133

RESULT 3
O8LTEL PRELIMINARY; PRT; 329 AA.
ID O8LTEL;
AC 08LTEL;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE A1 read-through protein (A1 protein).
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allolevivirus.
OX NCBI_Taxid=12009;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=14667253;
RA Bacher J.M., Bull J.J., Ellington A.D.;
RT "Evolution of phage with chemically ambiguous proteomes."
RL BMC Evol. Biol. 3:24-24(2003).
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.2%; Score 652; DB 2; Length 329;
Best Local Similarity 97.7%; Pred. No. 9.7e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRRNK 60
DB 2 AKLEVTTLGNIGKDGROTLVLPNGVNPPTNGVASISQAGAVPALEKRVTVSVSQPSRRNK 61
QY 61 NKVVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASPL 120
DB 62 NKVVQVKIQNPACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIQOLNPAY 132
DB 122 LIDAIQOLNPAY 133

RESULT 4
AAA16663 PRELIMINARY; PRT; 329 AA.
ID AAA16663;
AC AAA16663;
DT 02-MAR-2004 (TREMBlrel. 27, Created)

DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE A1 protein.
OS Bacteriophage Q-beta.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altollevivirub.
OX NCBI_TaxID=12009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94109687; PubMed=7506687;
RA Kozlovskaya T.M., Cielens I., Dreilima D., Dislers A., Baumanns V.,
Ose V., Pumpens P.;
RT "Recombinant RNA phage Q beta capsid particles synthesized and self-
assembled in Escherichia coli.";
RL Gene 137:133-137(1993).
DR EMBL; M99039; AAA16663.1; -;
SQ SEQUENCE 329 AA; 36134 MW; E0F30215A8C197CB CRC64;

Query Match 98.2%; Score 652; DB 2; Length 329;
Best Local Similarity 97.7%; Pred. No. 9,7e-55;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALKRYTVSVSOPSRNRK 60
DB 2 AKLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALKRYTVSVSOPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIIDQINPAY 132
DB 122 LIDAIIDQINPAY 133

RESULT 5
Q9TOR9 PRELIMINARY; PRT; 133 AA.
ID Q9TOR9;
AC Q9TOR9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altollevivirub.
OX NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14699.1; -;
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 2559593DAF6F6474 CRC64;

Query Match 84.8%; Score 563; DB 2; Length 133;
Best Local Similarity 82.6%; Pred. No. 1.4e-46;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ARLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALKRYTVSVSOPSRNRK 60
DB 2 AKLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALKRYTVSVSOPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIIDQINPAY 132
DB 122 LIDAIIDQINPAY 133

RESULT 6
O64307 PRELIMINARY; PRT; 329 AA.
ID O64307;
AC O64307;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE A1-protein.
OS Enterobacteria phage MX1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Altollevivirub.
OX NCBI_TaxID=75723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poort R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059242; AAC14700.1; -;
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35880 MW; 372B1DD5DB52F15 CRC64;

Query Match 84.8%; Score 563; DB 2; Length 329;
Best Local Similarity 82.6%; Pred. No. 4.1e-46;
Matches 109; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ARLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALKRYTVSVSOPSRNRK 60
DB 2 AKLEVTYIGNIGKDGROTLVLPNGVNPPTNGVASLSQAGAVPALKRYTVSVSOPSRNRK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 120
DB 62 NYKVQVKIQNPACTANGSCDPSVTRQKADVTFSFTQYSTDEERAFVTELAALLASPL 121
QY 121 LIDAIIDQINPAY 132
DB 122 LIDAIIDQINPAY 133

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RESULT 7
O9T0S0      PRELIMINARY; PRT; 133 AA.
ID 09T0S0;
AC 09T0S0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Coat protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
OX NCBI_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phase Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
DR Coat protein.
SQ SEQUENCE 133 AA; 14198 MW; 098722E3C63A255 CRC64;

Query Match      81.8%; Score 543; DB 2; Length 133;
Best Local Similarity 79.5%; Pred. No. 1.2e-44;
Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 ARLEVTITGNIQKGRQTLVLPNGVNPPTNGVVASISQAGAVPALERKRVTSVSQSSRRK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 AKLQAITISGICKKDDVTLIDNPRGVNPTNGVVAISQAGAVPALERKRVTSVSQSSRRK 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NYKVQVKIÖNPACTANGSCDPSVTRÖKADVTFSFTQYSTDEERAPVTELAALLASPL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 NYKVQVKIÖNPACTANGSCDPSVTRÖKADVTFSFTQYSTDEERAPVTELAALLADPM 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LIDAIÖLNPAV 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 LVNAIDNLNPAV 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
O64303      PRELIMINARY; PRT; 329 AA.
ID 064303;
AC 064303;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Al-protein.
OS Bacteriophage M11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
OX NCBI_TaxID=74336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;

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RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RNA phase Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052431; AAC06250.1; -.
DR HSSP; P03615; IOBE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF01819; Lev1_coat; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 329 AA; 35893 MW; 3E33CD821EE625F4 CRC64;

Query Match      81.8%; Score 543; DB 2; Length 329;
Best Local Similarity 79.5%; Pred. No. 3.5e-44;
Matches 105; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 ARLEVTITGNIQKGRQTLVLPNGVNPPTNGVVASISQAGAVPALERKRVTSVSQSSRRK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 AKLQAITISGICKKDDVTLIDNPRGVNPTNGVVAISQAGAVPALERKRVTSVSQSSRRK 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NYKVQVKIÖNPACTANGSCDPSVTRÖKADVTFSFTQYSTDEERAPVTELAALLASPL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 NYKVQVKIÖNPACTANGSCDPSVTRÖKADVTFSFTQYSTDEERAPVTELAALLADPM 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LIDAIÖLNPAV 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 LVNAIDNLNPAV 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
COAT_BPSP      STANDARD; PRT; 132 AA.
ID COAT_BPSP;
AC P09673;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Coat protein.
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirivirus.
OX NCBI_TaxID=12027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289362; PubMed=3399390;
RA Hirashima A., Hirose T., Inayama S., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
RL -1- FUNCTION: Forms the phage shell; binds to the phage RNA.
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CC -----
DR EMBL; X07489; CA30374.1; -.
DR HSSP; P03615; IOBE.

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DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein; RNA-binding.
SQ SEQUENCE 132 AA; 14129 MW; 50B1E6CC6AFOA254 CRC64;

Query Match 79.6%; Score 528.5; DB 1; Length 132;
Best Local Similarity 78.0%; Pred. No. 3.1e-43;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 ARLEVTYLGNGKDGQRTLVLPNGVNPNGVSLSGAGVPALEKRVTVSVSOPSRNK 60
DB 2 AKLNQVTLSTKIGKNDQTLTPRGVNPNGVASLSEGAVALERKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRKXADYTFSTQYSTDEBRAPVTELAALLASPL 120
DB 62 NFKVQIKQNPACTCRD-ACDPSVTRSAFADVTLSFTSYSTDEBRALIRTELAALLADPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 10
VAL_BPSP STANDARD; PRT; 331 AA.
AC P03677;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Readthrough protein A1 [Contains: Coat protein].
OS Bacteriophage SP.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus.
NCBI_TaxID=12027;
RX MEDLINE=88289362; PubMed=3399390;
RA Hirschma A., Hirose T., Inokuchi Y., Jacobson A.B.;
RT "Analysis of the complete nucleotide sequence of the group IV RNA
RT Coliphage SP.";
RL Nucleic Acids Res. 16:6205-6221(1988).
CC -1- FUNCTION: Not yet known.
CC -1- MISCELLANEOUS: The readthrough protein A1 includes the coat
CC protein sequence.

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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X07489; CAB37299.1; -
DR PIR; S01964; S01964.
DR HSSP; P03615; 10BE.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
FT CHAIN 1 132 Coat protein.
FT CHAIN 1 331 Readthrough protein A1.
SQ SEQUENCE 331 AA; 36203 MW; 4A6642B4B52C6582 CRC64;

Query Match 79.6%; Score 528.5; DB 1; Length 331;
Best Local Similarity 78.0%; Pred. No. 9e-43;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 ARLEVTYLGNGKDGQRTLVLPNGVNPNGVSLSGAGVPALEKRVTVSVSOPSRNK 60
DB 2 AKLNQVTLSTKIGKNDQTLTPRGVNPNGVASLSEGAVALERKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRKXADYTFSTQYSTDEBRAPVTELAALLASPL 120
DB 121 IYDAIDNINPAY 132

DB 62 NFKVQIKQNPACTCRD-ACDPSVTRSAFADVTLSFTSYSTDEBRALIRTELAALLADPL 120
QY 121 LIDAIDQINPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 11
O9TOR8 PRELIMINARY; PRT; 132 AA.
ID O9TOR8
AC O9TOR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major coat protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Allovirvirus.
NCBI_TaxID=75725;
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RT RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RT Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19(1996).
RN [3]

RP SEQUENCE FROM N.A.
RA Beekwilder M.J., Nieuwenhuizen R., van Duin J.;
RL Submitted (Apr-1998) to the EMBL/Genbank/DBS databases.
DR EMBL; AF059243; AAC14703.1; -
DR HSSP; P03615; 10BE.
DR GO; GO:0019028; C:cyt viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002703; Lev1_coat.
DR Pfam; PF01819; Lev1_coat; 1.
KW Coat protein.
SQ SEQUENCE 132 AA; 14143 MW; 67270937575F22EA CRC64;

Query Match 74.8%; Score 496.5; DB 2; Length 132;
Best Local Similarity 75.0%; Pred. No. 3.9e-40;
Matches 99; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 1 ARLEVTYLGNGKDGQRTLVLPNGVNPNGVSLSGAGVPALEKRVTVSVSOPSRNK 60
DB 2 AKLNQVTLSTKIGKNDQTLTPRGVNPNGVASLSEGAVALERKRVTVSVSOPSRNK 61
QY 61 NYKVQVKIQNPACTANGSCDPSVTRKXADYTFSTQYSTDEBRAPVTELAALLASPL 120
DB 62 NFKVQIKQNPACTCRD-ACDPSVTRSGSRDVTLSFTSYSTDEBRALIRTELAALLKDDL 120
QY 121 LIDAIDQINPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 12
O64310 PRELIMINARY; PRT; 330 AA.
ID O64310
AC O64310;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A1-Protein.
OS Enterobacteria phage NL95.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;

```

OC Allollevivirus.
OX NCBI_Taxid=75725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239761; PubMed=7723040;
RA Beekwilder M.U., Nieuwenhuizen R., van Duin J.;
RT "Secondary structure model for the last two domains of single-stranded
RN RNA phage Q beta.";
RL J. Mol. Biol. 247:903-917 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96190948; PubMed=8609616;
RA Beekwilder J., Nieuwenhuizen R., Poot R., van Duin J.;
RT "Secondary structure model for the first three domains of Q beta RNA.
RN Control of A-protein synthesis.";
RL J. Mol. Biol. 256:8-19 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Beekwilder M.U., Nieuwenhuizen R., van Duin J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059243; AAC14704.1; -.
DR HSSP; P03615; 10BB.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat_1.
DR PROSITE; PS00030; RM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 330 AA; 56175 MW; 961E5F408334410 CRC64;

Query Match
Best Local Similarity 74.8%; Score 496.5; DB 2; Length 330;
Matches 99; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

OY 1 ALEVTYTGNIKDGQGTALNPRGVNPTNGVASISQAGAVPALEKRTVSVSQPSRRNK 60
DB 2 ALCNKVTLTGIGAGAGQTLTLPRGVNPTNGVASISEAGVPALEKRTVSVSQPSRRNK 61
OY 61 NYKVQVQKIONPACTANGSCDPSVTFRQKADYVFSFYQSTDEERAFVTELAALIASPL 120
DB 62 NYKVQVQKIONPACTANGSCDPSVTFRQKADYVFSFYQSTDEERAFVTELAALIASPL 120
OY 121 LIDAIDQINPAY 132
DB 121 IYDAIDNINPAY 132

RESULT 13
COAT_BPPRR STANDARD; PRT; 131 AA.
AC P03616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Coat protein.
OS Bacteriophage PR1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC unclassified Leviviridae.
OX NCBI_Taxid=12024;
RN [1]
RP SEQUENCE.
RX MEDLINE=79148387; PubMed=107028;
RA Dhasee P., Vandeckerckhove J., van Montagu M.;
RT "The primary structure of the coat protein of the broad-host-range RNA
RN bacteriophage PR1.";
RL Eur. J. Biochem. 94:375-386 (1979).
CC 1- FUNCTION: Forms the phage shell; binds to the phage RNA.
DR InterPro; IPR002703; Levi_coat.
DR Pfam; PF01819; Levi_coat_1.
KW Coat protein; direct protein sequencing; RNA-binding.
SQ SEQUENCE 131 AA; 14535 MW; E7E639F1E50FC612 CRC64;

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Query Match
Best Local Similarity 17.5%; Score 116; DB 1; Length 131;
Matches 42; Conservative 14; Mismatches 58; Indels 16; Gaps 5;

OY 17 QTLVNLPRGVNPT-----NGVASISQAGAVPALEKRTVSVSQPSRRNKRYKVQV 66
DB 4 QNLVVKDRATFNDHTFPFRDIRDVGVEVSTGVPIGSRPTSLRKTSNGR--YKSTL 61
OY 67 KIQNPT--ACTANGSCDPSVTFRQKADYVFSFYQSTDEER-AFVTELAALIASPLLI- 122
DB 62 KLVPEVVGQTVNGVTVTPVAVTSTVTVDFDADASTTKERNFVGMADALKADLMVH 121
OY 123 DAIDQINPAY 132
DB 122 DTIVNLQGVY 131

RESULT 14
Q8VDC2 PRELIMINARY; PRT; 473 AA.
AC Q8VDC2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane protein 7.
GN Name=Trmem7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Liver;
RA MEDLINE=22350095; PubMed=12461651;
RA Kise H., Darai E., Kise C., Kost-Alimova M., Klein G., Dumanek J.P.,
RA Imreh S.;
RT "Comparative human/murine sequence analysis of the common eliminated
RT region 1 from human 3p21.3.";
RL Mamm. Genome 13:646-655 (2002).
DR EMBL; AJ428064; CAD20986.1; -.
DR MGD; MGI:2446841; Trmem7.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
SQ SEQUENCE 473 AA; 51994 MW; B1872B0EB69F2A4D CRC64;

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Query Match
Best Local Similarity 14.5%; Score 96.5; DB 2; Length 473;
Matches 45; Conservative 18; Mismatches 45; Indels 69; Gaps 7;

OY 5 TVTLGNIGKDGQGTIV-----LNPRGVNPTNG--VASISQAGAVP-----ALEK 46
DB 195 TATCSNIISSQPSKVPQASKANPQASNPKNPKVSCSKPPAPLPSLTSAREP 254
OY 47 RVTYVSGPSRRNKRYKVQV-----KIQNPT-----ACTANGSCDPSVTRQ----- 87
DB 255 KVTYVCSNIISSRSSSKVQMPQASRVNPQTSNPTNPKISCTSKSPSTPRLLTIQQLSV 314
OY 88 -----KVADYVFSFYQSTDEERAFVTELAALIASPLLI 122
DB 315 SPPAPAPTCVIOMSPPTPIDGSRADVAKENTRSKTPK-----ALLSSPLLYV 361

RESULT 15
TACY_LISSE STANDARD; PRT; 530 AA.
AC P31830;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Seeligiolysin precursor (Thiol-activated cytolysin).
GN Name=Igo;
OS Listeria seeligieri.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

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OK NCBI_TaxID=1640;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLCC;
RX MEDLINE=92162018; PubMed=1543752;
RA Haas A., Dumbeky M., Kieft J.;
RT "Listeriolysin genes: complete sequence of ilo from Listeria ivanovi
and of iso from Listeria seeligeri.";
RL Biochim. Biophys. Acta 1130:81-84(1992).
CC -!- FUNCTION: Sulfhydryl-activated toxin. Is able to lyse cholesterol
containing membranes. Can be reversibly inactivated by oxidation.
Cholesterol is the receptor for the binding of these toxins to
eukaryotic cell membranes.
CC -!- SIMILARITY: Belongs to the thiol-activated cytolysin family.
CC -----
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CC -----
CC EMBL; X60462; CAA42996.1; -
CC PIR; S22340; S22340.
DR HSSP; P19995; 1PFO.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PR01400; TACTTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
KW Cytolysis; Hemolysis; Lipid-binding; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 530
FT SITE 485 485 Binding to cholesterol (By similarity).
SQ SEQUENCE 530 AA; 59181 MW; 416F7A4D02029866 CRC64;

Query Match 13.5%; Score 89.5; DB 1; Length 530;
Best Local Similarity 25.0%; Pred. No. 5.2; Mismatches 37; Indels 43; Gaps 7;
Matches 34; Conservative 22;

QY 13 KDGRTLVL--NPRGVNPT-----NGVASLSQAG-----VPALKRV 48
DB 94 KDGSEYIVVEKKKGINNNADISVINAISSLTYPGALVKANRELVENQPNVLPVKRDL 153
QY 49 TVSVSQPSNRKRYVQVKTQNPFTACTANGSCDPSYTR--QKY-----ADVTFSPFQ 98
DB 154 TLSVDLPQMTKKDKNKIFVK--NPTKSNVNNAVNTLVERWMDKYSKAYPNINKIDYS--- 208
QY 99 YSTDERAFVRTTELAA 114
DB 209 ----DEMAISESQTIA 220

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